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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:22:56 ; Search time 103.05 Seconds
(without alignments)
743.120 Million cell updates/sec

Title: US-09-575-580B-4
Perfect score: 1048
Sequence: 1 MEEVDLQPLSATIACHLDP.....RPKXIIQTRPEYTPHLS 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	198	5	AAE18911 Human MCI
2	1002.5	95.7	197	5	AAE18915 Human MCI
3	1002.5	95.7	197	8	ADR14119 Human NF-
4	1002.5	95.7	252	7	ADB64738 Human pro
5	920.5	87.8	198	5	AAE18912 Mouse MCI
6	872.5	83.3	197	5	AAE18914 Human MCI
7	872.5	83.3	197	7	ADR25770 Human pro
8	847.5	80.9	242	8	ADR10481 Human pro
9	835.5	79.7	171	2	AAW73898 Human Dow
10	620.5	59.2	234	4	AAB31788 Amino aci
11	620.5	59.2	243	7	ADB64062 Human pro
12	620.5	59.2	255	5	AAW50760 Human Dow
13	620.5	59.2	255	7	ADR37339 Human Dow
14	613.5	58.5	197	5	AAE18913 Mouse MCI
15	609.5	58.2	197	6	ABO07172 Human p33
16	596.5	56.9	192	5	AAE18916 Human MCI
17	596.5	56.9	192	7	ADR37341 Human Dow
18	596	56.9	241	5	AAE18917 Human MCI
19	596	56.9	241	6	ABO07173 Human p53
20	596	56.9	241	7	ADR37342 Human Dow
21	595	56.8	212	5	AAE18918 Human MCI
22	497	47.4	142	3	AAW58452 Lung can
23	439	41.9	111	3	AAW01768 Human sec
24	379.5	36.2	292	4	ABB71467 Drosophil
25	284	27.1	58	4	AAW15671 Peptide #

ALIGNMENTS

RESULT 1

AAE18911
ID AAE18911 standard; protein; 198 AA.
XX AC AAE18911;
XX AC AAE18911;
DT 17-MAY-2002 (first entry)
XX Human MCIP associated protein #2.
DE Human MCIP associated protein #2.
XX Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;
KW heart failure; cardiomyopathy; heart disease; human.
XX Homo sapiens.
XX WO200204491-A2.
XX 17-JAN-2002.
XX 06-JUL-2001; 2001WO-US021662.
XX 07-JUL-2000; 2000US-0216601P.
XX 13-FEB-2001; 2001US-00782953.
XX (TEXA) UNIV TEXAS SYSTEM.
XX (WILL//) WILLIAMS S R.
XX (ROTH//) ROTHERMEL B.
XX Williams SR, Rothermel B;
XX WPI: 2002-179698/23.
XX N-PSDB; AAD30152.
XX Screening for modulators of muscle calcineurin interacting protein (MCIP) binding, expression or phosphorylation, useful for treating cardiac hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a test compound.

Disclosure; Page 148-149; 174pp; English.

The invention relates to muscle calcineurin interacting proteins (MCIPs) and nucleic acid molecules encoding such proteins. MCIPs form a physical complex with the catalytic subunit of calcineurin and increased levels of MCIPs correspond to a reduced ability of calcineurin to stimulate to transcriptions of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for treating cardiac hypertrophy and heart failure.

CC Antibodies to MCIP can be used in characterising the MCIP content of
 CC healthy and diseased tissues and subsequently for determining the
 CC presence or absence of cardiomyopathy or as predictor of heart disease.
 CC The present sequence is human MCIP associated protein
 XX
 XX Sequence 198 AA;
 SQ
 Query Match 100.0%; Score 1048; DB 5; Length 198;
 Best Local Similarity 100.0%; Pred. No. 7.3e-108;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEEVDLQDLPSATIAIACHLDPRVFDGLCRKAFESLRTYDKDTTFQYFKSFRVRINFSN 60
 Db 1 MEEVDLQDLPSATIAIACHLDPRVFDGLCRKAFESLRTYDKDTTFQYFKSFRVRINFSN 60
 QY 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQV 120
 Db 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQV 120
 QY 121 EDATPVINDLLYAIKSLGPGKGYELHAATDPTPSVVHVCSDDQNEEEEMERMKRP 180
 Db 121 EDATPVINDLLYAIKSLGPGKGYELHAATDPTPSVVHVCSDDQNEEEEMERMKRP 180
 QY 181 KPKIOTRRPEYTPIHLS 198
 Db 181 KPKIOTRRPEYTPIHLS 198
 RESULT 2
 AAE18915
 ID AAE18915 standard; protein; 197 AA.
 XX
 AC AAE18915;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Human MCIP associated protein #2.
 XX
 KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;
 KW heart failure; cardiomyopathy; heart disease; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200204491-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 06-JUL-2001; 2001WO-US021662.
 XX
 PR 07-JUL-2000; 2000US-0216601P.
 PR 13-FEB-2001; 2001US-00782953.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (WILL/) WILLIAMS S R.
 PA (ROTH/) ROTHERMEL B.
 XX
 PI Williams SR, Rothermel B;
 XX
 DR WPI; 2002-179698/23.
 DR N-PSDB; AAD30156.
 XX
 PT Screening for modulators of muscle calcineurin interacting protein (MCIP)
 PT binding, expression or phosphorylation, useful for treating cardiac
 PT hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a
 PT test compound.
 XX
 XX Example 1; Page 161-162; 174pp; English.
 XX
 CC The invention relates to muscle calcineurin interacting proteins (MCIPs)
 CC and nucleic acid molecules encoding such proteins. MCIPs form a physical
 CC complex with the catalytic subunit of calcineurin and increased levels of
 CC MCIPs correspond to a reduced ability of calcineurin to stimulate
 CC transcription of certain target genes. The invention also relates to

CC methods for identifying modulators of MCIP binding, expression or
 CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin
 CC may be used for treating cardiac hypertrophy and heart failure.
 CC Antibodies to MCIP can be used in characterising the MCIP content of
 CC healthy and diseased tissues and subsequently for determining the
 CC presence or absence of cardiomyopathy or as predictor of heart disease.
 CC The present sequence is human MCIP associated protein. Note: This
 CC sequence has been described as murine MCIP splice variant in the
 CC specification, however the sequence seems to be a MCIP associated protein
 XX
 XX Sequence 197 AA;
 SQ
 Query Match 95.7%; Score 1002.5; DB 5; Length 197;
 Best Local Similarity 96.5%; Pred. No. 8.4e-103;
 Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 QY 1 MEEVDLQDLPSATIAIACHLDPRVFDGLCRKAFESLRTYDKDTTFQYFKSFRVRINFSN 60
 Db 1 MEEVDLQDLPSATIAIACHLDPRVFDGLCRKAFESLRTYDKDTTFQYFKSFRVRINFSN 60
 QY 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQV 120
 Db 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQV 120
 QY 121 EDATPVINDLLYAIKSLGPGKGYELHAATDPTPSVVHVCSDDQNEEEEMERMKRP 180
 Db 121 EDATPVINDLLYAIKSLGPGKGYELHAATDPTPSVVHVCSDDQNEEEEMERMKRP 180
 QY 181 KPKIOTRRPEYTPIHLS 198
 Db 180 KPKIOTRRPEYTPIHLS 197
 RESULT 3
 ADRI4119
 ID ADRI4119 standard; protein; 197 AA.
 XX
 AC ADRI4119;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Human NF-kappaB pathway-associated protein SeqID120.
 XX
 KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
 KW immunosuppressive; vulnery; gene therapy; immune disorder;
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
 KW viral replication; host cell survival; evasion of immune response;
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW autoimmune disorder; hyper immune activity;
 KW aberrant acute phase response; hypercongenital condition; birth defect;
 KW necrotic lesion; wound; organ transplant rejection;
 KW aberrant signal transduction; proliferating disorder; cancer;
 KW HIV propagation; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2004065577-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 13-JAN-2004; 2004WO-US000798.
 XX
 PR 14-JAN-2003; 2003US-0440068P.
 PR 12-MAY-2003; 2003US-0469757P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.

QY 11 SATIACHLDPVFDGLCRAKFESLRTYDKDTTFQYFKSKVRINFSNPLSAADARLR 70
Db 11 SSLIACVANSDFSESETRAKFESLRTYDKDTTFQYFKSKVRINFSNPLSAADARLQ 70
QY 71 LHKTEFLGKEMKLYFAQTLHGSSHLAPPNDKQFLISPPASPPVGWKQVEDATPVINYD 130
Db 71 LHKTEFLGKEMKLYFAQTLHGSSHLAPPNDKQFLISPPASPPVGWKQVEDATPVINYD 130
QY 131 LLYAISKLGPGEKYLHAATDPTPSVVHVCSDDQNEEEEMERMKRPKPKIIOTRRP 190
Db 131 LLYAISKLGPGEKYLHAATDPTPSVVHVCSDDQNEEEEMERMKRPKPKIIOTRRP 189
QY 191 EYTPHLS 198
Db 190 EYTPHLS 197
RESULT 7
ADE25770
ID ADE25770 standard; protein; 197 AA.
AC ADE25770;
XX
DT 29-JAN-2004 (first entry)
DE Human protein differentially expressed in foam cells #47.
KW Human; differential expression; foam cell; LPS; lipopolysaccharide;
KW cardiovascular disease; atherosclerosis.
OS Homo sapiens.
PN US2003194721-A1.
PD 16-OCT-2003.
PF 18-SEP-2002; 2002US-00247671.
PR 19-SEP-2001; 2001US-0323784P.
XX (INCY-) INCYTE GENOMICS INC.
PI Mikita T, Shiffman D, Porter JG, Kaser MR;
XX WPI; 2003-875398/81.
DR N-PSDB; ADE25696.
XX
PT Combination containing several polynucleotide that are differentially
PT expressed in foam cells and complements of the polynucleotides, useful
PT for diagnosing cardiovascular disease or atherosclerosis.
XX
PS Disclosure; SEQ ID NO 174; 37pp; English.
XX
CC The invention relates to a combination comprising several polynucleotides
CC having any one of 127 sequences (S1) such as the sequence of human
CC calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4
CC hydrolase, human CGI-142 protein mRNA, human K+ channel beat 2 subunit
CC mRNA, etc., and their complements. The cDNAs are differentially expressed
CC in LPS (lipopolysaccharide)-treated foam cells. Also included are
CC obtaining an extended or full length gene from a library of nucleic acid
CC sequences, an expression vector containing the nucleic acids, a host cell
CC containing the vector, a purified polypeptide appearing as ADE25750 and
CC ADE25751, producing a protein by culturing the host cell, and a
CC composition comprising a purified antibody that specifically binds to the
CC proteins. The foam cell-expressed nucleic acids are useful for a high
CC throughput detection of differential expression of one or more
CC polynucleotides in a sample. The sample is from a subject with
CC atherosclerosis and comparison with a standard defines early, mid or late
CC stages of the disorder. The foam cell-expressed nucleic acids are useful
CC to identify a ligand which binds a polynucleotide. The library is chosen
CC from DNA molecules, peptides, proteins and RNA molecules. The protein is
CC useful for a high throughput screening of library of molecules or

CC compounds to identify at least one ligand which specifically binds a
CC protein, for purifying a ligand from a sample for making an antibody. The
CC foam cell-expressed nucleic acids are useful for diagnosing
CC cardiovascular disorder. The foam cell-expressed nucleic acids are useful
CC as elements on a microarray which can be used for detecting related
CC polynucleotide in a sample, diagnosing cardiovascular disease,
CC atherosclerosis. The present sequence represents a protein differentially
CC expressed in LPS treated foam cells.
XX
SQ Sequence 197 AA;
Query Match 83.3%; Score 872.5; DB 7; Length 197;
Best Local Similarity 89.4%; Pred. No. 2.5e-88;
Matches 168; Conservative 7; Mismatches 12; Indels 1; Gaps 1;
QY 11 SATIACHLDPVFDGLCRAKFESLRTYDKDTTFQYFKSKVRINFSNPLSAADARLR 70
Db 11 SSLIACVANSDFSESETRAKFESLRTYDKDTTFQYFKSKVRINFSNPLSAADARLQ 70
QY 71 LHKTEFLGKEMKLYFAQTLHGSSHLAPPNDKQFLISPPASPPVGWKQVEDATPVINYD 130
Db 71 LHKTEFLGKEMKLYFAQTLHGSSHLAPPNDKQFLISPPASPPVGWKQVEDATPVINYD 130
QY 131 LLYAISKLGPGEKYLHAATDPTPSVVHVCSDDQNEEEEMERMKRPKPKIIOTRRP 190
Db 131 LLYAISKLGPGEKYLHAATDPTPSVVHVCSDDQNEEEEMERMKRPKPKIIOTRRP 189
QY 191 EYTPHLS 198
Db 190 EYTPHLS 197
RESULT 8
ADR10481
ID ADR10481 standard; protein; 242 AA.
AC ADR10481;
XX
DT 04-NOV-2004 (first entry)
DE Human protein useful for treating neurological disease Seq 3987.
XX
KW human; oligo-capping method; diagnostic marker; gene therapy;
KW osteoporosis; neurological disease; Alzheimer's disease;
KW Parkinson's disease; dementia; short memory; cancer;
KW sense or motor function; emotional reaction; fear response; panic;
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;
KW tranquiliser.
OS Homo sapiens.
PN EP1447413-A2.
PD 18-AUG-2004.
XX
PF 12-FEB-2004; 2004EP-00003145.
PR 14-FEB-2003; 2003JP-00102207.
PR 09-MAY-2003; 2003JP-00131452.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
PI Wakamatsu A, Ishii S, Nagai K, Irie R;
XX WPI; 2004-583265/57.
DR N-PSDB; ADR10442.
XX
PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX Claim 1; SEQ ID NO 3987; 2686pp; English.
XX


```
XX PD 18-JAN-2001.
XX OS
XX PF
XX PN 06-JUL-2000; 2000WO-US018509.
XX XX
XX PD 07-JUL-1999; 99US-0142678P.
XX XX
XX PA (INCY-) INCYTE GENOMICS INC.
XX XX
XX PI Tang YT, Yue H;
XX XX
XX DR WPI; 2001-147193/15.
XX DR N-PSDB; AAF25338.
XX XX
XX PT New human detoxification protein and polynucleotide, useful for
XX PT diagnosis, prevention and treatment of autoimmune/inflammatory disorders
XX PT and cell proliferative disorders including cancer.
XX XX
XX PS Claim 1; Page 77; 79pp; English.
XX XX
XX CC The present sequence represents a human detoxification polypeptide
XX CC (DETX). DETX and its (ant)agonists are useful for preventing or treating
XX CC disorders associated with decreased or increased expression or activity
XX CC of DETX. DETX polypeptides are useful for screening compounds that
XX CC specifically binds to DETX and for identifying (ant)agonists. Diseases
XX CC prevented, treated and diagnosed include cancers (e.g. leukaemia,
XX CC melanoma, adenocarcinoma, cancers of the brain, bone marrow, breast,
XX CC kidney, liver, pancreas, prostate and uterus), autoimmune/inflammatory
XX CC disorders (e.g. rheumatoid arthritis, asthma, atherosclerosis, autoimmune
XX CC thyroiditis, psoriasis and ulcerative colitis), bacterial, fungal,
XX CC parasitic infections and cell proliferative disorders (e.g. actinic
XX CC keratosis, arteriosclerosis, cirrhosis and hepatitis). Anti-DETX
XX CC antibodies may be used as antagonists, as a targeting or delivery
XX CC mechanism for bringing pharmaceutical agents into contact with cells or
XX CC tissues expressing DETX and for diagnosis of DETX-related disorders
XX SQ
XX Sequence 234 AA;
XX
XX Query Match 59.2%; Score 620.5; DB 4; Length 234;
XX Best Local Similarity 62.4%; Pred. No. 3.6e-60;
XX Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;
XX
XX QY 5 DLQDLPSATIACHLDPRVFDGLCRKPFESLFRDYKDTTFQYFKSFRKVRINFNSPLSA 64
XX Db 42 DFNDLPNSLFACNVHQSVFEGESKEKFEGLFRDYDCCVTFQLFKSFRRVRINFNSPKA 101
XX
XX QY 65 ADARLRLHKTFLGKEMKLYFAQTLHGSS-----HLAPNDPKQFLISPPASPPVGVKOV 120
XX Db 102 ARARIELHETQFRGKKLKYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSPPPVGVQPI 161
XX
XX QY 121 EDATPVINYDLYAISKLGPGKELHAATDTPSVVHVCSDOENEEEMERMKRP 180
XX Db 162 NDATPVINYDLYAVAKGPGKELHAGTESTPSVVHVCDSDIEEDDPK-----TSP 216
XX
XX QY 181 KPKIIQTRRPEYTP 194
XX Db 217 KPKIIQTRRGLPP 230
XX
XX RESULT 11
XX ID ADB64062
XX AC ADB64062 standard; protein; 243 AA.
XX XX
XX XX 04-DEC-2003 (first entry)
XX XX
XX DE Human protein encoded by clone BRAHW20014590.
XX XX
XX KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
XX KW cell regeneration; membrane protein; signal transduction-related protein;
XX KW transcription-related protein; osteoporosis; neurological disease;
XX KW cancer; tumour.
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XX XX Homo sapiens.
XX OS
XX PN EP1308459-A2.
XX XX
XX PD 07-MAY-2003.
XX XX
XX PF 28-MAR-2002; 2002EP-00007401.
XX XX
XX PR 05-NOV-2001; 2001JP-00379298.
XX PR 25-JAN-2002; 2002US-00350978.
XX XX
XX PA (HELI-) HELIX RES INST.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX XX
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX DR WPI; 2003-450961/43.
XX DR N-PSDB; ADS62092.
XX XX
XX PT New polynucleotides and polypeptides, useful for developing a diagnostic
XX PT marker or medicines for regulation of their expression and activity, or
XX PT as targets of gene therapy.
XX XX
XX PS Claim 1; Page; 222pp; English.
XX XX
XX CC The invention discloses a polynucleotide comprising a sequence selected
XX CC from 1970 fully defined nucleotide sequences which encode novel
XX CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
XX CC or its partial peptide, an antibody binding to the polypeptide or peptide
XX CC of the polynucleotide, immunologically assaying the polypeptide or
XX CC peptide of the polynucleotide by contacting the polypeptide or peptide
XX CC with the antibody of the encoded protein, and observing the binding
XX CC between the two, a transformant carrying the polynucleotide in an
XX CC expressible manner and an antisense polynucleotide. The oligonucleotide
XX CC is useful as a primer for synthesising the polynucleotide, or as a probe
XX CC for detecting the polynucleotide. The polynucleotides and encoded
XX CC proteins are useful as pharmaceutical agents and many disease-related
XX CC genes may be included in them, for developing a diagnostic marker or
XX CC medicines for regulation of their expression and activity, or as targets
XX CC of gene therapy. The genes are involved in tissue and/or cell
XX CC regeneration. Membrane proteins, signal transduction-related proteins,
XX CC transcription-related proteins, disease-related proteins and genes
XX CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
XX CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
XX CC the activity or expression of the encoded protein to treat diseases. The
XX CC sequence presented is a protein of the invention. Note: Some of the
XX CC sequence data for this patent is not represented in the printed
XX CC specification, but is based on sequence information supplied by the
XX CC European Patent Office.
XX SQ
XX Sequence 243 AA;
XX
XX Query Match 59.2%; Score 620.5; DB 7; Length 243;
XX Best Local Similarity 62.4%; Pred. No. 3.8e-60;
XX Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;
XX
XX QY 5 DLQDLPSATIACHLDPRVFDGLCRKPFESLFRDYKDTTFQYFKSFRKVRINFNSPLSA 64
XX Db 51 DFNDLPNSLFACNVHQSVFEGESKEKFEGLFRDYDCCVTFQLFKSFRRVRINFNSPKA 110
XX
XX QY 65 ADARLRLHKTFLGKEMKLYFAQTLHGSS-----HLAPNDPKQFLISPPASPPVGVKOV 120
XX Db 111 ARARIELHETQFRGKKLKYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSPPPVGVQPI 170
XX
XX QY 121 EDATPVINYDLYAISKLGPGKELHAATDTPSVVHVCSDOENEEEMERMKRP 180
XX Db 171 NDATPVINYDLYAVAKGPGKELHAGTESTPSVVHVCDSDIEEDDPK-----TSP 225
XX
XX QY 181 KPKIIQTRRPEYTP 194
XX |||||
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Db	226	KPKIIQTRRPGLPP	239
RESULT 12			
AAM50760			
ID	AAM50760	standard; protein; 255 AA.	
XX			
AC	AAM50760;		
XX			
DT	18-APR-2002	(first entry)	
XX			
DE	Human Down syndrome critical region 1-like 1 protein.		
XX			
KW	Down syndrome critical region 1-like 1; DSCR1L1 alpha; human;		
KW	Down syndrome; Alzheimer's disease; dementia; transgenic;		
KW	neuroprotective; nontropic; anticonvulsant; diagnosis; therapy.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 11	/note= "encoded by TNG"	
FT	Domain	129..199	
FT	Region	169..176	
FT		/note= "ISPPXSP box"	
XX	WO200204513-A2.		
XX			
PD	17-JAN-2002.		
XX			
PF	11-JUL-2001; 2001WO-US021982.		
XX			
PR	11-JUL-2000; 2000US-00614474.		
XX			
PA	(INCY-) INCYTE GENOMICS INC.		
XX			
PI	Loring JF, Tingley DW, Edwards CM, Streeter DG;		
XX			
DR	WPI; 2002-164633/21.		
DR	N-PSDB; ABA91457.		
XX			
PT	Novel Down syndrome critical region 1-like 1 protein and nucleic acid		
PT	encoding the protein useful for diagnosis and treatment of Alzheimer's		
PT	disease, Down syndrome and other forms of dementia.		
XX			
PS	Claim 1; Page 47-49; 54pp; English.		
XX			
CC	The present sequence is that of novel Down syndrome critical region 1-		
CC	like 1 protein (DSCR1L1 alpha). Northern analysis indicated expression of		
CC	DSCR1L1 alpha in various libraries, with the highest abundance in tissues		
CC	from the nervous system, including tissues associated with schizophrenia,		
CC	Huntington's disease, epilepsy and amyotrophic lateral sclerosis. An		
CC	absence of DSCR1L1 expression was observed in 7 of 8 libraries from		
CC	subjects with Alzheimer's disease. A claimed method for detecting		
CC	differential expression of a nucleic acid encoding DSCR1L1 alpha can be		
CC	used to diagnose Down syndrome, Alzheimer's disease and other forms of		
CC	dementia. The purified DSCR1L1 alpha protein, or a portion of it, can be		
CC	used to identify ligands which specifically bind the protein, such as a		
CC	DNA or RNA molecule, peptide nucleic acid, peptide, protein, mimetic,		
CC	agonist, antagonist, antibody, immunoglobulin inhibitor or drug, for use		
CC	as a therapeutic. The protein can also be used to raise antibodies useful		
CC	in diagnosis and therapy		
XX			
SQ	Sequence 255 AA;		
Query Match	59.2%;	Score 620.5;	DB 5; Length 255;
Best Local Similarity	62.4%;	Pred. No. 4.1e-60;	
Matches 121;	Conservative 22;	Mismatches 42;	Indels 9; Gaps 2;
QY	5	DIQDLPSATIACHLDPFRVFDGLCRAKFESLFRYDKDTTFQYFKSFKRVRINFNPLSA	64
Db	63	DPNDLPNSLFAACNVHQSVEGESKEFGLFRYDCCVTFQLFKSFRVRINFNPKSA	122

QY	65	ADARLRLHKTEFLGKEMKLYFAQTTHIGSS-----HLAPNPDKQFLISPPASPPVGWKQV	120
Db	123	ARARIELHETQPRGKKLKLKLYFAQVTPETDGDGKHLAPPQAKQFLISPPSPVGVQPI	182
QY	121	EDATPVINYDLIYALSKLPGKEKYEHLHAATDTPSPVVHVHVCSDQENEESEEMERMKP	180
Db	183	NDATPVLNLYLLYAVAKLPGKEKYEHLHAGTESTPSPVVHVHVCSDIEEDDPK-----TSP	237
QY	181	KPKIIQTRRPEYTP	194
Db	238	KPKIIQTRRPGLPP	251
RESULT 13			
ADE37339			
ID	ADE37339	standard; protein; 255 AA.	
XX			
AC	ADE37339;		
XX			
DT	29-JAN-2004	(first entry)	
XX			
DE	Human Down syndrome critical region 1-like 1alpha protein.		
XX			
KW	Down syndrome critical region 1-like 1alpha protein; nontropic;		
KW	neuroprotective; peptide therapy; gene therapy; Alzheimer's disease;		
KW	human.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 11	/label= OTHER	
FT		/note= "OTHER= Unknown or other amino acid; encoded by	
FT		TNG"	
XX			
PN	US2003186333-A1.		
XX			
PD	02-OCT-2003.		
XX			
PF	06-NOV-2002; 2002US-00290438.		
XX			
PR	11-JUL-2000; 2000US-00614474.		
XX			
PA	(INCY-) INCYTE GENOMICS INC.		
XX			
PI	Loring JF, Tingley DW, Edwards CM, Streeter DG;		
XX			
DR	WPI; 2003-811734/76.		
DR	N-PSDB; ADE37338.		
XX			
PT	New purified Down syndrome critical region 1-like 1 protein, used for		
PT	diagnosing and treating Alzheimers disease, and for identifying and		
PT	purifying antibodies that specific bind to the protein.		
XX			
PS	Example 8; Fig 1; 39pp; English.		
XX			
CC	This invention relates to a novel purified Down syndrome critical region		
CC	1-like 1 protein comprising a polypeptide having fully defined sequence		
CC	of 255 amino acids, as given in the specification. Compounds which		
CC	modulate the protein of the invention may have nontropic or		
CC	neuroprotective activity. The protein sequence of the invention and the		
CC	CDNA sequence which encodes it may be useful for peptide therapy and gene		
CC	therapy respectively. The invention may prove useful in development of		
CC	therapeutics for the treatment of Alzheimer's disease. The present		
CC	sequence is the amino acid sequence of the human Down syndrome critical		
CC	region 1-like 1alpha protein of the invention. Note: This sequence is		
CC	given as Seq ID2 in the sequence listing but is referred to as Seq ID1		
CC	throughout the specification.		
XX			
SQ	Sequence 255 AA;		
Query Match	59.2%;	Score 620.5;	DB 7; Length 255;

Best Local Similarity 62.4%; Pred. No. 4.1e-60;
Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;

QY 5 DLQDLSATACHLDRVFDGLCRAKFESLFTYDKDTTFQYFKSKVRINFNSPLSA 64
Db 63 DFNDLNSLFPACNVHVSFEGESKKEFGLFTYDDCVTFQYFKSKVRINFNSPKSA 122
QY 65 ADARLRLHTEFLGKEMKLYFAQTLHIGSS----HLAPPNDKQFLISPPASPPVGVKQV 120
Db 123 ARARIELHETQFGKKLYFAQVOTPETDGLKHLAPQPAKQFLISPPSPVGVQPI 182
QY 121 EDATPVINDLLVAISKLGEGKVELHAATDPTSPVVHVHVCSDQNEEEEMERMRKP 180
Db 183 NDATPVNLVNDLLYAVAKLGEGKVELHAGTSTPSVVHVHVCSDIEBEDPK-----TSP 237
QY 181 KPKIOTRRPEYTP 194
Db 238 KPKIOTRRPGLPP 251

RESULT 14
AAE18913
ID AAE18913 standard; protein; 197 AA.
XX
AC AAE18913;
XX
DT 17-MAY-2002 (first entry)
XX
DE Mouse MCIP associated proein #4.
XX
KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;
KW heart failure; cardiomyopathy; heart disease; mouse.
XX
OS Mus musculus.

XX
PN WO200204491-A2.
XX
PD 17-JAN-2002.
XX
PF 06-JUL-2001; 2001WO-US021662.
XX
PR 07-JUL-2000; 2000US-0216601P.
PR 13-FEB-2001; 2001US-00782953.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (WILL/) WILLIAMS S R.
PA (ROTH/) ROTHERMEL B.
XX
PI Williams SR, Rothermel B;
XX
DR WPI; 2002-179698/23.
DR N-PSDB; AAD30154.

XX
PT Screening for modulators of muscle calcineurin interacting protein (MCIP)
PT binding, expression or phosphorylation, useful for treating cardiac
PT hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a
PT test compound.

XX
PS Disclosure; Page 154; 174pp; English.
XX
CC The invention relates to muscle calcineurin interacting proteins (MCIPs)
CC and nucleic acid molecules encoding such proteins. MCIPs form a physical
CC complex with the catalytic subunit of calcineurin and increased levels of
CC MCIPs correspond to a reduced ability of calcineurin to stimulate
CC transduction of certain target genes. The invention also relates to
CC methods for identifying modulators of MCIP binding, expression or
CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin
CC may be used for treating cardiac hypertrophy and heart failure.
CC Antibodies to MCIP can be used in characterizing the MCIP content of
CC healthy and diseased tissues and subsequently for determining the
CC presence or absence of cardiomyopathy or as predictor of heart disease.
CC The present sequence is mouse MCIP associated protein. Note: This
CC sequence has been described as mouse MCIP2 encoding DNA in the

CC specification, however the sequence seems to be a MCIP associated protein
XX
SQ Sequence 197 AA;

Query Match 58.5%; Score 613.5; DB 5; Length 197;
Best Local Similarity 63.3%; Pred. No. 1.7e-59;
Matches 119; Conservative 22; Mismatches 38; Indels 9; Gaps 2;

QY 11 SATIACHLDRPVFDGLCRAKFESLFTYDKDTTFQYFKSKVRINFNSPLSAADARLR 70
Db 11 STLAVCVDFVFTNVEVKEKFEGLFTYDDCVTFQYFKSKVRINFNSPKSAARARIE 70
QY 71 LHKTEFLGKEMKLYFAQTLHIGSS----HLAPPNDKQFLISPPASPPVGVKQVDPV 126
Db 71 LHETQFRGKKLYFAQVOTPETDGLKHLAPQPAKQFLISPPSPVGVKQVDPV 130
QY 127 INYDLLYAIKLGEGKVELHAATDPTSPVVHVHVCSDQNEEEEMERMRKPQKI 186
Db 131 LNYDLLYAVAKLGEGKVELHAGTSTPSVVHVHVCSDMEBEDPK-----TSPKPIIQ 185
QY 187 TRRPEYTP 194
Db 186 TRRPGGLPP 193

RESULT 15
ABO07172
ID ABO07172 standard; protein; 197 AA.
XX
AC ABO07172;
XX
DT 13-AUG-2003 (first entry)
XX
DE Human p53 modifying protein, SEQ ID 132.

XX
KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
KW antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
KW apoptotic disorder; cell proliferation disorder.

XX
OS Homo sapiens.
XX
PN WO2002099122-A1.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017382.
XX
PR 05-JUN-2001; 2001US-0296076P.
PR 10-OCT-2001; 2001US-0328605P.
PR 15-FEB-2002; 2002US-0357253P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
XX
DR WPI; 2003-156859/15.
DR N-PSDB; ACD13348.

XX
PT Identifying modulators of the p53 pathway for use in treating apoptotic
PT or cell proliferation disorders, comprises screening for agents that
PT modulate activity of a human ortholog of genes that modify the p53
PT pathway in Drosophila.

XX
PS Example 2; Page 434-435; 678pp; English.
XX
CC The invention relates to identifying (M1) a candidate p53 pathway
CC modulating agent, by contacting an assay system comprising a purified HM
CC polypeptide (human orthologue of genes that modify the p53 pathway in
CC Drosophila) or nucleic acid with a test agent under conditions, where but
CC for the presence of the test agent, the system provides a reference
CC activity, and detecting a test agent-biased activity of the assay system.
CC Also included are modulating (M2) a p53 pathway of a cell (comprising

contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid sequence, where p53 function is restored), modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with a probe for HM expression; (c) comparing the results with a control; and (d) determining whether the comparison indicates a likelihood disease). (M1) is useful for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. Modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell proliferation disorders (e.g. cancer). Another two new methods (M2 and M3) are useful for modulating the p53 pathway of a cell, thus restoring the p53 function of the cell, so that the cell undergoes normal proliferation or progression through the cell cycle. (M2) and (M3) are also useful for treating defects in the p53 pathway such as angiogenic, apoptotic or cell proliferation disorders. The present sequence represents a human p53 pathway modifying protein

Sequence 197 AA;

Search completed: November 16, 2005, 16:47:31
Job time : 106.05 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:22:55 ; Search time 27 Seconds
(without alignments)
547.426 Million cell updates/sec

Title: US-09-575-580B-4
Perfect score: 1048
Sequence: 1 MEEVDLQDLPSTAIACHLDP.....RPKPKIIQTRRPEYTPIHLS 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	847.5	80.9	171	4 US-09-949-016-6493	Sequence 6493, Ap
2	847.5	80.9	173	4 US-09-949-016-11053	Sequence 11053, A
3	835.5	79.7	171	2 US-08-665-040-2	Sequence 2, Appl
4	620.5	59.2	255	4 US-09-614-474-2	Sequence 2, Appl
5	609.5	58.2	206	4 US-09-949-016-11450	Sequence 11450, A
6	596.5	56.9	192	4 US-09-614-474-10	Sequence 10, Appl
7	596.5	56.9	192	4 US-09-949-016-6659	Sequence 6659, Ap
8	596	56.9	241	4 US-09-614-474-11	Sequence 11, Appl
9	596	56.9	248	4 US-09-949-016-7081	Sequence 7081, Ap
10	439	41.9	111	4 US-09-513-999C-5849	Sequence 5849, Ap
11	372.5	35.5	289	4 US-09-270-767-44503	Sequence 44503, A
12	90.5	8.6	4019	4 US-09-854-133-425	Sequence 425, Ap
13	88	8.4	284	5 PCT-US94-09752-4	Sequence 4, Appl
14	86.5	8.3	822	4 US-09-641-734-3	Sequence 3, Appl
15	84.5	8.1	719	4 US-09-641-741-28	Sequence 28, Appl
16	83	7.9	367	4 US-09-248-796A-15492	Sequence 15492, A
17	82	7.8	1128	4 US-09-641-741-30	Sequence 30, Appl
18	82	7.8	1128	4 US-09-060-482-8	Sequence 8, Appl
19	81	7.7	1128	1 US-08-111-939-2	Sequence 2, Appl
20	80	7.6	314	4 US-09-328-352-5324	Sequence 5324, Ap
21	80	7.6	492	4 US-09-792-024-91	Sequence 91, Appl
22	79	7.5	708	4 US-09-949-016-7574	Sequence 7574, Ap
23	79	7.5	1132	1 US-08-446-038B-18	Sequence 18, Appl
24	79	7.5	1132	1 US-08-446-010B-18	Sequence 18, Appl
25	79	7.5	1132	2 US-08-805-445-18	Sequence 18, Appl
26	79	7.5	1132	2 US-08-064-067D-18	Sequence 18, Appl
27	79	7.5	1132	2 US-09-066-208-18	Sequence 18, Appl

28	79	7.5	1142	1 US-08-097-997A-11	Sequence 11, Appl
29	79	7.5	1142	3 US-08-665-574C-11	Sequence 11, Appl
30	79	7.5	1142	3 US-08-946-994-11	Sequence 11, Appl
31	79	7.5	1154	1 US-08-357-598-7	Sequence 7, Appl
32	79	7.5	1154	1 US-08-446-010B-24	Sequence 24, Appl
33	79	7.5	1154	2 US-09-003-289-7	Sequence 7, Appl
34	79	7.5	1154	4 US-09-963-137-203	Sequence 203, Appl
35	79	7.5	1154	5 PCT-US95-16435-7	Sequence 7, Appl
36	78.5	7.5	547	4 US-09-877-730-26	Sequence 26, Appl
37	78.5	7.5	624	4 US-09-877-730-24	Sequence 24, Appl
38	78.5	7.5	628	4 US-09-877-730-30	Sequence 30, Appl
39	78.5	7.5	712	4 US-09-877-730-22	Sequence 22, Appl
40	78.5	7.5	793	4 US-09-877-730-28	Sequence 28, Appl
41	78.5	7.5	826	4 US-09-877-730-16	Sequence 16, Appl
42	78.5	7.5	864	4 US-09-883-096-2	Sequence 2, Appl
43	78.5	7.5	904	4 US-09-877-730-6	Sequence 6, Appl
44	78.5	7.5	907	4 US-09-877-730-20	Sequence 20, Appl
45	78.5	7.5	985	4 US-09-877-730-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-6493
; Sequence 6493, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6493
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6493

Query Match 80.9%; Score 847.5; DB 4; Length 171;
Best Local Similarity 95.9%; Pred. No. 7.8e-90;
Matches 162; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
QY 30 AKFESLFRTYDQDTTFQFKSKFRVIRNFSNPLSAADARLRLHKTFLGKMKLYFAQTL 89
DB 4 AKFESLFRTYDQDTTFQFKSKFRVIRNFSNPLSAADARLRLHKTFLGKMKLYFAQTL 63
QY 90 HGSSHLAPPNDKQFLISPPASPPVGWKQVDATPVINDLLYATSKLGPGEKYLHAA 149
DB 64 HGSSHLAPPNDKQFLISPPASPPVGWKQVDATPVINDLLYATSKLGPGEKYLHAA 123

QY 150 TDPTSVVVHVHCESQENEBEEMERMRPKPKIIQTRRPEYTPIHLS 198
DB 124 TTTTTSVVHVHCESDOE-KEEEEEMERMRPKPKIIQTRRPEYTPIHLS 171

RESULT 2

US-09-949-016-11053
; Sequence 11053, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

```
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11053
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11053

Query Match      80.9%; Score 847.5; DB 4; Length 173;
Best Local Similarity 95.9%; Pred. No. 7.9e-90;
Matches 162; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 30 AKFESLFRITYDKDTTFQYFKSPKRVINFSNPLSAADARLRLHKTFLGKEMKLYFAQTL 89
Db 6 AKFESLFRITYDKDTTFQYFKSPKRVINFSNPLSAADARLRLHKTFLGKEMKLYFAQTL 65
QY 90 HIGSSLAPPNDPKQFLISPPASPPVGWQVEDATPVINYDILLYAISKLGPGEKYLHAA 149
Db 66 HIGSSLAPPNDPKQFLISPPASPPVGWQVEDATPVINYDILLYAISKLGPGEKYLHAA 125
QY 150 TDPTPSVVHVHVCESDOENEEEMERMKRPKPKIIQTRRPEYTPIHLS 198
Db 126 TDTTPSVVVHVHVCESDQE-KEEEEMERMRPKPKIIQTRRPEYTPIHLS 173

RESULT 3
US-08-665-040-2
; Sequence 2, Application US/08665040
; Patent No. 5869318
; GENERAL INFORMATION:
; APPLICANT: ESTIVILL PALLEJA, XAVIER
; APPLICANT: FUENTES, JUAN JOSE
; APPLICANT: PRITCHARD, MELANIE
; TITLE OF INVENTION: A NEW GENE SEQUENCE OF THE
; TITLE OF INVENTION: DOWN SYNDROM CRITICAL REGION OF HUMAN CHROMOSOME 21,
; TITLE OF INVENTION: IDENTIFIED BY A NEW "ALU-SPLICING PCR" TECHNIQUE,
; TITLE OF INVENTION: CODING FOR A PROLINE-RICH PROTEIN (DSCRI) HIGHLY
; TITLE OF INVENTION: EXPRESSED IN FOETEL BRAIN AND IN HEART AND METHOD
; TITLE OF INVENTION: FOR CHARACTERIZING IT.
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LADAS & PARRY
; STREET: 26 WEST 61ST STREET
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1 FOR DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,040
; FILING DATE: JUNE 7, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: ES P9501140
; FILING DATE: JUNE 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: JANET I. CORD
; REGISTRATION NUMBER: 33,778
; REFERENCE/DOCKET NUMBER: U010815-9
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-665-040-2

Query Match      79.7%; Score 835.5; DB 2; Length 171;
Best Local Similarity 94.7%; Pred. No. 1.9e-88;
Matches 160; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 30 AKFESLFRITYDKDTTFQYFKSPKRVINFSNPLSAADARLRLHKTFLGKEMKLYFAQTL 89
Db 4 AKFESLFRITYDKDTTFQYFKSPKRVINFSNPLSAADARLRLHKTFLGKEMKLYFAQTL 63
QY 90 HIGSSLAPPNDPKQFLISPPASPPVGWQVEDATPVINYDILLYAISKLGPGEKYLHAA 149
Db 64 HIGSSLAPPNDPKQFLISPPASPPVGWQVEDATPVINYDILLYAISKLGPGEKYLHAA 123
QY 150 TDPTPSVVHVHVCESDOENEEEMERMKRPKPKIIQTRRPEYTPIHLS 198
Db 124 TDTTPSVVVHVHVCESDQE-KEEEEMERMRPKPKIIQTRRPEYTPIHLS 171

RESULT 4
US-09-614-474-2
; Sequence 2, Application US/09614474
; Patent No. 6524819
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS
; FILE REFERENCE: PC-0013 US
; CURRENT APPLICATION NUMBER: US/09/614,474
; CURRENT FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: incyte ID No. 6524819 247500.5
; NAME/KEY: unsure
; LOCATION: 11
; OTHER INFORMATION: unknown or other
; US-09-614-474-2

Query Match      59.2%; Score 620.5; DB 4; Length 255;
Best Local Similarity 62.4%; Pred. No. 2.5e-63;
Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;

QY 5 DLQDLPSATIAIHLDPVDFVGLCPAKFESLFRITYDKDTTFQYFKSPKRVINFSNPLSA 64
Db 63 DFNDLPNLFACNVHQSVFEGEESKEFGLFRITYDKDTTFQYFKSPKRVINFSNPKSA 122
QY 65 ADARLRLHKTFLGKEMKLYFAQTLHIGSS----HLAPPNDPKQFLISPPASPPVGWQV 120
Db 123 ARARIELHETQFRGKKLYFAQVQTPETDGDGKLHLAPPQAKQFLISPPSSPPVGWQPI 182
QY 121 EDATPVINYDILLYAISKLGPGEKYLHAAATPTPSVVHVHVCESDOENEEEMERMKRP 180
Db 183 NDATPVLNYDILLYAVAKLGPGEKYLHAGTSTPSVVHVHVCSDIEEDDPK-----TSP 237
QY 181 KPDKIIQTRRPEYTP 194
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Db 238 KPQIIQTRRPLGP 251

RESULT 5

US-09-949-016-11450

; Sequence 11450, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11450

; LENGTH: 206

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-11450

Query Match 58.2%; Score 609.5; DB 4; Length 206;

Best Local Similarity 63.3%; Pred. No. 3.4e-62;

Matches 119; Conservative 21; Mismatches 39; Indels 9; Gaps 2;

QY 11 SATIACHLDPRVVDGLCRKAFESLRTYDQDTTFOYFKSKFRVRINFSNPLSAADARLR 70

Db 20 STLVCVVDVEFTNQEVKEFGGLFRTYDQDTTFOYFKSKFRVRINFSNPKSAARARIE 79

QY 71 LHKTEFLGKEMKLYFAQTLLHIGSS----HLAPPNDKQFLISPPASPPVGVKQVEDATPV 126

Db 80 LHETQFRGKKLYFAQVQTPETDGDGKLHAPPQPAKQFLISPPSPVGVQWQINDATPV 139

QY 127 INYDLLYAIKSLGPGKEKYLHAATDTPSVVVHVCSDOENEEEMERMKRKPQKIIQ 186

Db 140 LNYDLLYAVAKLGPGEKYLHAGTSTPSVVHVCDSDIEEDDPK-----TSPKPKIIQ 194

QY 187 TRPEYTP 194

Db 195 TRRPLGP 202

RESULT 6

US-09-614-474-10

; Sequence 10, Application US/09614474

; Patent No. 6524819

; GENERAL INFORMATION:

; APPLICANT: Loring, Jeanne F.

; APPLICANT: Tingley, Debra W.

; APPLICANT: Edwards, Carla M.

; APPLICANT: Streeter, David G.

; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS

; FILE REFERENCE: PC-0013 US

; CURRENT APPLICATION NUMBER: US/09/614,474

; CURRENT FILING DATE: 2000-07-11

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PERL Program

; SEQ ID NO 10

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6524819 g1435040

US-09-614-474-10

Query Match 56.9%; Score 596.5; DB 4; Length 192;

Best Local Similarity 62.2%; Pred. No. 9.8e-61;

Matches 117; Conservative 21; Mismatches 41; Indels 9; Gaps 2;

QY 11 SATIACHLDPRVVDGLCRKAFESLRTYDQDTTFOYFKSKFRVRINFSNPLSAADARLR 70

Db 6 STLVCVVDVEFTNQEVKEFGGLFRTYDQDTTFOYFKSKFRVRINFSNPKSAARARIE 65

QY 71 LHKTEFLGKEMKLYFAQTLLHIGSS----HLAPPNDKQFLISPPASPPVGVKQVEDATPV 126

Db 66 LHETQFRGKKLYFAQVQTPETDGDGKLHAPPQPAKQFLISPPSPVGVQWQINDATPV 125

QY 127 INYDLLYAIKSLGPGKEKYLHAATDTPSVVVHVCSDOENEEEMERMKRKPQKIIQ 186

Db 126 LNYDLLYAVAKLGPGEKYLHAGTSTPSVVHVCDSDIEEDDPK-----TSPKPKIIQ 180

QY 187 TRPEYTP 194

Db 181 TRRPLGP 188

RESULT 7

US-09-949-016-6659

; Sequence 6659, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6659

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-6659

Query Match 56.9%; Score 596.5; DB 4; Length 192;

Best Local Similarity 62.2%; Pred. No. 9.8e-61;

Matches 117; Conservative 21; Mismatches 41; Indels 9; Gaps 2;

QY 11 SATIACHLDPRVVDGLCRKAFESLRTYDQDTTFOYFKSKFRVRINFSNPLSAADARLR 70

Db 6 STLVCVVDVEFTNQEVKEFGGLFRTYDQDTTFOYFKSKFRVRINFSNPKSAARARIE 65

QY 71 LHKTEFLGKEMKLYFAQTLLHIGSS----HLAPPNDKQFLISPPASPPVGVKQVEDATPV 126

Db 66 LHETQFRGKKLYFAQVQTPETDGDGKLHAPPQPAKQFLISPPSPVGVQWQINDATPV 125

QY 127 INYDLLYAIKSLGPGKEKYLHAATDTPSVVVHVCSDOENEEEMERMKRKPQKIIQ 186

Db 126 LNYDLLYAVAKLGPGEKYLHAGTSTPSVVHVCDSDIEEDDPK-----TSPKPKIIQ 180

QY 187 TRPEYTP 194

Db 181 TRRPLGP 188

RESULT 8

US-09-614-474-11

; Sequence 11, Application US/09614474

; Patent No. 6524819

; GENERAL INFORMATION:

; APPLICANT: Loring, Jeanne F.

```
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS
; FILE REFERENCE: PC-0013 US
; CURRENT APPLICATION NUMBER: US/09/614,474
; CURRENT FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6524819 g6017919
US-09-614-474-11

Query Match          56.9%; Score 596; DB 4; Length 241;
Best Local Similarity 61.9%; Pred. No. 1.6e-60;
Matches 120; Conservative 20; Mismatches 44; Indels 10; Gaps 2;

QY      2  EVDVLDLPSATIAACHLDPRVFDGLCRAKFESLFRITYDKDTTFQYKFSKVRINFNSP 61
Db      38  EMDVLDLPSLTSFACSVHAEVFEAREQKRFALFTYDDQVTFQKFSFRVRINFNSP 97

QY      62  LSAADARLRLHKTFLGKEMKLYFAQTLHIG----SSHLAPPNDPKQLISPPASPPVGW 117
Db      98  EAAARARIELHETDFNGKLYFAQVMSGEVRDQKSYLLPPQPKQLISPPASPPVGW 157

QY      118  QVEDATPVINDLLYALSKLGPGEKYELHAATDTPSPVVHVCSDDQNEEEEMERM 177
Db      158  QKSEDAMPVINDLLCAVSKLGPGEKYELHAGTESTPSPVVHVCSSETEEE-----T 211

QY      178  KRPKKIIQTRRP 191
Db      212  KNPKQKIAQTRRPD 225

RESULT 9
US-09-949-016-7081
; Sequence 7081, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7081
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7081

Query Match          56.9%; Score 596; DB 4; Length 248;
Best Local Similarity 61.9%; Pred. No. 1.6e-60;
Matches 120; Conservative 20; Mismatches 44; Indels 10; Gaps 2;

QY      2  EVDVLDLPSATIAACHLDPRVFDGLCRAKFESLFRITYDKDTTFQYKFSKVRINFNSP 61
Db      45  EMDVLDLPSLTSFACSVHAEVFEAREQKRFALFTYDDQVTFQKFSFRVRINFNSP 104

QY      62  LSAADARLRLHKTFLGKEMKLYFAQTLHIG----SSHLAPPNDPKQLISPPASPPVGW 117

; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS
; FILE REFERENCE: PC-0013 US
; CURRENT APPLICATION NUMBER: US/09/614,474
; CURRENT FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6524819 g6017919
US-09-614-474-11

Query Match          56.9%; Score 596; DB 4; Length 241;
Best Local Similarity 61.9%; Pred. No. 1.6e-60;
Matches 120; Conservative 20; Mismatches 44; Indels 10; Gaps 2;

QY      2  EVDVLDLPSATIAACHLDPRVFDGLCRAKFESLFRITYDKDTTFQYKFSKVRINFNSP 61
Db      38  EMDVLDLPSLTSFACSVHAEVFEAREQKRFALFTYDDQVTFQKFSFRVRINFNSP 97

QY      62  LSAADARLRLHKTFLGKEMKLYFAQTLHIG----SSHLAPPNDPKQLISPPASPPVGW 117
Db      98  EAAARARIELHETDFNGKLYFAQVMSGEVRDQKSYLLPPQPKQLISPPASPPVGW 157

QY      118  QVEDATPVINDLLYALSKLGPGEKYELHAATDTPSPVVHVCSDDQNEEEEMERM 177
Db      158  QKSEDAMPVINDLLCAVSKLGPGEKYELHAGTESTPSPVVHVCSSETEEE-----T 211

QY      178  KRPKKIIQTRRP 191
Db      212  KNPKQKIAQTRRPD 225

RESULT 10
US-09-513-999C-5849
; Sequence 5849, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5849
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5849

Query Match          41.9%; Score 439; DB 4; Length 111;
Best Local Similarity 84.2%; Pred. No. 7.2e-43;
Matches 85; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY      11  SATIACHLDPRVFDGLCRAKFESLFRITYDKDTTFQYKFSKVRINFNSPLSAADARLR 70
Db      11  SSLIACVANSDFSESETRAKFESLFRITYDKDTTFQYKFSKVRINFNSPFAADARLR 70

QY      71  LHKTEFLGKEMKLYFAQTLHIGSSHLAPPNDPKQLISPPA 111
Db      71  LHKTEFLGKEMKLYFAQTLHIGSSHLAPPNDPKQLISPPA 111

RESULT 11
US-09-270-767-44503
; Sequence 44503, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44503
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44503

Query Match          35.5%; Score 372.5; DB 4; Length 289;
Best Local Similarity 43.8%; Pred. No. 1.4e-34;
Matches 71; Conservative 38; Mismatches 48; Indels 5; Gaps 3;

QY      3  EVD---LQDLPSATIAACHLDPRVFDGLCRAKFESLFRITYDKDTTFQYKFSKVRINFNS 59
Db      111  EVDADSFDDLTSIIVNIHSEVFANPELKHAMELFTFSESATFQWLRSFRRLRVNYD 170
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RESULT 13
PCT-US94-09752-4
; Sequence 4, Application PC/TUS9409752
; GENERAL INFORMATION:
; APPLICANT: David S. Strayer and Avinaash Chander
; TITLE OF INVENTION: Compositions and Methods for
; TARGETING CELLS AND MODULATING PULMONARY SURFACTANT SECRETION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09752
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/176.218

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RESULT 15
US-09-641-741-28
; Sequence 28, Application US/09641741
; Patent No. 6420155
; GENERAL INFORMATION:
; APPLICANT: Kerry E. Quinn
; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids
; TITLE OF INVENTION: encoding Same
; FILE REFERENCE: 15966-581
; CURRENT APPLICATION NUMBER: US/09/641,741
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/159,613
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: 60/175,534
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/224,086
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-641-741-28

Query Match      8.1%; Score 84.5; DB 4; Length 719;
Best Local Similarity 21.8%; Pred. No. 1.1;
Matches 31; Conservative 27; Mismatches 37; Indels 47; Gaps 7;

QY 54 VRINFSNPLSAADARLRLHKTFF---LGKMKLYFAQTLHGSSHLAPPNDKQFLISPP 110
Db 585 LRVDPSPWTPQQRMRQRRQLQVRLMRREQMRL---RRLNSTAGPATSPTP---ALMEPP 637
QY 111 ASP-----PVGWK--QVEDATPVINVDLLYAIKLGPGGEKYLHAATDPT 153
Db 638 PSFTPAITLRPWELVLTPTTTAGWEESETETYTEVVT-----EFETGYGTD-- 681
QY 154 PSVVHVHCESDOENEEEEEEME 175
Db 682 ----LEVEIEEEEEEEEND 699
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Search completed: November 16, 2005, 16:31:56
Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:22:57 ; Search time 100.8 Seconds
(without alignments)
821.875 Million cell updates/sec

Title: US-09-575-580B-4
Perfect score: 1048
Sequence: 1 MEEVDLQDLPSTAIACHLDP.....RPKPKIOTRRPEYTPHLS 198

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Searched: 1867879 seqs, 418409474 residues
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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9: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1048	100.0	198	US-09-782-953-3 Sequence 3, Appli
2	1048	100.0	198	US-09-782-953-4 Sequence 4, Appli
3	1002.5	95.7	197	US-09-782-953-15 Sequence 15, Appli
4	1002.5	95.7	197	US-09-782-953-16 Sequence 16, Appli
5	1002.5	95.7	197	US-10-755-889-120 Sequence 120, App
6	1002.5	95.7	252	US-10-104-047-2892 Sequence 2892, Ap
7	920.5	87.8	198	US-09-782-953-6 Sequence 6, Appli
8	920.5	87.8	198	US-09-782-953-7 Sequence 7, Appli
9	872.5	83.3	197	US-09-782-953-12 Sequence 12, Appli
10	872.5	83.3	197	US-09-782-953-13 Sequence 13, Appli
11	872.5	83.3	197	US-10-247-671-174 Sequence 174, App

12	847.5	80.9	171	15	US-10-428-487-24	Sequence 24, Appli
13	620.5	59.2	243	15	US-10-104-047-2216	Sequence 2216, Ap
14	620.5	59.2	255	14	US-10-290-438-2	Sequence 2, Appli
15	613.5	58.5	197	9	US-09-782-953-9	Sequence 9, Appli
16	613.5	58.5	197	9	US-09-782-953-10	Sequence 10, Appli
17	596.5	56.9	192	9	US-09-782-953-18	Sequence 18, Appli
18	596.5	56.9	192	9	US-09-782-953-19	Sequence 19, Appli
19	596.5	56.9	192	14	US-10-290-438-10	Sequence 10, Appli
20	596.5	56.9	197	18	US-10-764-425-126	Sequence 126, App
21	596	56.9	241	9	US-09-782-953-21	Sequence 21, Appli
22	596	56.9	241	9	US-09-782-953-22	Sequence 22, Appli
23	596	56.9	241	14	US-10-290-438-11	Sequence 11, Appli
24	595	56.8	212	9	US-09-782-953-24	Sequence 24, Appli
25	595	56.8	212	9	US-09-782-953-25	Sequence 25, Appli
26	497	47.4	142	9	US-09-925-302-790	Sequence 790, App
27	497	47.4	142	10	US-09-925-302-790	Sequence 790, App
28	379.5	36.2	292	20	US-11-097-143-41193	Sequence 41193, A
29	284	27.1	58	9	US-09-864-761-35379	Sequence 35379, A
30	284	27.1	58	9	US-09-864-761-43076	Sequence 43076, A
31	271.5	25.9	56	9	US-09-864-761-34111	Sequence 34111, A
32	136.5	13.0	32	14	US-10-194-155-8	Sequence 8, Appli
33	94	9.0	699	16	US-10-437-963-186586	Sequence 186586,
34	93	8.9	227	16	US-10-437-963-196664	Sequence 196664,
35	92	8.8	513	15	US-10-282-122A-48629	Sequence 48629, A
36	92	8.8	1455	18	US-10-511-698-114	Sequence 114, App
37	90.5	8.6	4019	9	US-09-738-973-425	Sequence 425, App
38	90.5	8.6	4019	9	US-09-854-133-425	Sequence 425, App
39	90.5	8.5	4019	14	US-10-144-649A-425	Sequence 425, App
40	89.5	8.5	915	15	US-10-276-774-2443	Sequence 2443, Ap
41	87.5	8.3	1477	20	US-11-097-143-12672	Sequence 12672, A
42	86.5	8.3	822	9	US-09-824-734-3	Sequence 3, Appli
43	86.5	8.3	822	16	US-10-749-386-3	Sequence 3, Appli
44	86	8.2	915	16	US-10-437-963-132441	Sequence 132441,
45	85	8.1	2816	15	US-10-240-145-145	Sequence 145, App

ALIGNMENTS

RESULT 1
US-09-782-953-3
; Sequence 3, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSD:674P21
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-782-953-3

Query Match	100.0%	Score 1048;	DB 9;	Length 198;
Best Local Similarity	100.0%	Pred. No. 9.9e-97;		
Matches 198;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MEEVDLQDLPSTAIACHLDP	RVFVDGLCRAKESLFRTYDKDTTQYFKSKRVRINFSN	60
Db	1	MEEVDLQDLPSTAIACHLDP	RVFVDGLCRAKESLFRTYDKDTTQYFKSKRVRINFSN	60
Qy	61	PLSAADARLRLHKTFLKEMKLYFAQTUHGSSHLAPPNDPKQFLISPPASPPVGWQV	120	
Db	61	PLSAADARLRLHKTFLKEMKLYFAQTUHGSSHLAPPNDPKQFLISPPASPPVGWQV	120	

Qy	121	EDATPVNYDLYIAISKLGPEKYLHAATDTPSVVHVVCSDOENEENEEMRMKRP	180
Db	121	EDATPVNYDLYIAISKLGPEKYLHAATDTPSVVHVVCSDOENEENEEMRMKRP	180
Qy	181	KPKIIQTRRPETPIHLS	198
Db	181	KPKIIQTRRPETPIHLS	198

RESULT 2
 US-09-782-953-4
 ; Sequence 4, Application US/09782953
 ; Patent No. US20020150953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WILLIAMS, R. SANDERS
 ; APPLICANT: ROTHERMEL, BEVERLY
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
 ; TITLE OF INVENTION: CAUCINEURIN INTERACTING PROTEIN (MC1P)
 ; FILE REFERENCE: UTSD:674PZ1
 ; CURRENT APPLICATION NUMBER: US/09/782,953
 ; CURRENT FILING DATE: 2001-02-13
 ; PRIOR APPLICATION NUMBER: 60/216,601
 ; PRIOR FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 198
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-782-953-4

Query Match	100.0%; Score 1048; DB 9; Length 198;
Best Local Similarity	100.0%; Pred. No. 9.9e-97;
Matches 198; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MEEVDLQDLP SATTACHLDPRVFDGLCRAFESLFRTYDKDTTFQYKFSKRVINFSN 60
Db	1 MEEVDLQDLP SATTACHLDPRVFDGLCRAFESLFRTYDKDTTFQYKFSKRVINFSN 60
Qy	61 PLSAADARLR LHKEFTFLGEMKLYFAQTPLHTGSSHLAPPNDPKQLISPPASPVPVGWQKV 120
Db	61 PLSAADARLR LHKEFTFLGEMKLYFAQTPLHTGSSHLAPPNDPKQLISPPASPVPVGWQKV 120
Qy	121 EDATPVNI D LLYAI SKLGPEKVELHAATDPTPSVVHVHVCSDOENEEEEERMMKRP 180
Db	121 EDATPVNI D LLYAI SKLGPEKVELHAATDPTPSVVHVHVCSDOENEEEEERMMKRP 180
Qy	181 KP KIIOTRRP EYTPPI HLS 198
Db	181 KP KIIOTRRP EYTPPI HLS 198

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RESULT 3
US-09-782-953-15
; Sequence 15, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSD:674PZ1
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 15
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-953-15

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[illegible]

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RESULT 4
US-09-782-953-16
; Sequence 16, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSD:674PZ1
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-953-16

```

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RESULT 5
US 10 755-889-120
; Sender 120 Application US/10755889
; Publication No US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY

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; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-120

Query Match      95.7%; Score 1002.5; DB 16; Length 197;
Best Local Similarity 96.5%; Pred. No. 3.6e-92;
Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MEEVDLQDLP SATIACHLDP RVFV DGLCRAKFESLFR TYDKD TTFQYFKSFKRVRINFSN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEEVDLQDLP SATIACHLDP RVFV DGLCRAKFESLFR TYDKD TTFQYFKSFKRVRINFSN 60

QY 61 PL SAADARLRLHKTEFLGKEMKLYFAQTLHGSSHLAPPNPKQFLISPPASPPVGWKQV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PF SAADARLQLHKTEFLGKEMKLYFAQTLHGSSHLAPPNPKQFLISPPASPPVGWKQV 120

QY 121 EDATPVINVDLLYALSKLGPGEKLYELHAATDTPSVVVHVCSDDQNEEESEEMERMKRP 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 EDATPVINVDLLYALSKLGPGEKLYELHAATDTPSVVVHVCSDDQ-KSEEEEMERMRP 179

QY 181 KP KIIQTRRPEYTPIHLS 198
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 KP KIIQTRRPEYTPIHLS 197

RESULT 6
US-10-104-047-2892
; Sequence 2892, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2892
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2892

Query Match      95.7%; Score 1002.5; DB 15; Length 252;
Best Local Similarity 96.5%; Pred. No. 5e-92;
Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MEEVDLQDLP SATIACHLDP RVFV DGLCRAKFESLFR TYDKD TTFQYFKSFKRVRINFSN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 56 MEEVDLQDLP SATIACHLDP RVFV DGLCRAKFESLFR TYDKD TTFQYFKSFKRVRINFSN 115

QY 61 PL SAADARLRLHKTEFLGKEMKLYFAQTLHGSSHLAPPNPKQFLISPPASPPVGWKQV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 PF SAADARLQLHKTEFLGKEMKLYFAQTLHGSSHLAPPNPKQFLISPPASPPVGWKQV 175

QY 121 EDATPVINVDLLYALSKLGPGEKLYELHAATDTPSVVVHVCSDDQNEEESEEMERMKRP 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 176 EDATPVINVDLLYALSKLGPGEKLYELHAATDTPSVVVHVCSDDQ-KSEEEEMERMRP 234

QY 181 KP KIIQTRRPEYTPIHLS 198
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Db 235 KP KIIQTRRPEYTPIHLS 252

RESULT 7
US-09-782-953-6
; Sequence 6, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: UTSD:674P21
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-782-953-6

Query Match      87.8%; Score 920.5; DB 9; Length 198;
Best Local Similarity 89.9%; Pred. No. 6.2e-84;
Matches 178; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

QY 4 VDLQDLP---SATIACHLDP RVFV DGLCRAKFESLFR TYDKD TTFQYFKSFKRVRINFSN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MDRFRDPSYNFSSLIACVANDVFSSEYFAKESLFR TYDKD TTFQYFKSFKRVRINFSN 60

QY 61 PL SAADARLRLHKTEFLGKEMKLYFAQTLHGSSHLAPPNPKQFLISPPASPPVGWKQV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 PL SAADARLRLHKTEFLGKEMKLYFAQTLHGSSHLAPPNPKQFLISPPASPPVGWKQV 120

QY 121 EDATPVINVDLLYALSKLGPGEKLYELHAATDTPSVVVHVCSDDQNEEESEEMERMKRP 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 EDATPVINVDLLYALSKLGPGEKLYELHAATDTPSVVVHVCSDDQNEEESEEMERMKRP 180

QY 181 KP KIIQTRRPEYTPIHLS 198
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 KP KIIQTRRPEYTPIHLS 198

RESULT 8
US-09-782-953-7
; Sequence 7, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: UTSD:674P21
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-782-953-7

Query Match      87.8%; Score 920.5; DB 9; Length 198;
Best Local Similarity 89.9%; Pred. No. 6.2e-84;
Matches 178; Conservative 5; Mismatches 12; Indels 3; Gaps 1;
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QY 4 VDLQDLP---SATIACHLDPRVFDGLCRAKFESLRTYDKDITTFQYFKSFKRVRINFSN 60
Db 1 MFDPRFSYFSSLIACVANDVDFSESETRAKFESLRTYDKDITTFQYFKSFKRVRINFSN 60
QY 61 PLSAADARLRLHKTEFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVGWKQV 120
Db 61 PLSAADARLRLHKTEFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVGWKQV 120
QY 121 EDATPVINYDLIYAIKLGPGKGYELHAATDTPPSVVHVHVCSDQENEEEMERMKRP 180
Db 121 EDATPVINYDLIYAIKLGPGKGYELHAATDTPPSVVHVHVCSDQENEEEMERMKRP 180
QY 181 KPQIOTRRPEYTPHLS 198
Db 181 KPQIOTRRPEYTPHLS 198

RESULT 9
US-09-782-953-12
; Sequence 12, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSD:674PZ1
; CURRENT APPLICATION NUMBER: US/09/782,953
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-953-12

Query Match 83.3%; Score 872.5; DB 9; Length 197;
Best Local Similarity 89.4%; Pred. No. 4e-79;
Matches 168; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 11 SATIACHLDPRVFDGLCRAKFESLRTYDKDITTFQYFKSFKRVRINFSNPLSAADARLR 70
Db 11 SSSIACVANSDFSESETRAKFESLRTYDKDITTFQYFKSFKRVRINFSNPFSAADARLQ 70
QY 71 LHKTEFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVGWKQVEDATPVINYD 130
Db 71 LHKTEFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVGWKQVEDATPVINYD 130
QY 131 LLYAISKLGPGKGYELHAATDTPPSVVHVHVCSDQENEEEMERMKRPKPKIIQTRRP 190
Db 131 LLYAISKLGPGKGYELHAATDTPPSVVHVHVCSDQENEEEMERMKRPKPKIIQTRRP 189
QY 191 EYTPHLS 198
Db 190 EYTPHLS 197

RESULT 11
US-10-247-671-174
; Sequence 174, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 174
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 5511889CD1
US-10-247-671-174

Query Match 83.3%; Score 872.5; DB 14; Length 197;
Best Local Similarity 89.4%; Pred. No. 4e-79;
Matches 168; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 11 SATIACHLDPRVFDGLCRAKFESLRTYDKDITTFQYFKSFKRVRINFSNPLSAADARLR 70
Db 11 SSSIACVANSDFSESETRAKFESLRTYDKDITTFQYFKSFKRVRINFSNPFSAADARLQ 70
QY 71 LHKTEFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVGWKQVEDATPVINYD 130
Db 71 LHKTEFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVGWKQVEDATPVINYD 130
QY 131 LLYAISKLGPGKGYELHAATDTPPSVVHVHVCSDQENEEEMERMKRPKPKIIQTRRP 190
Db 131 LLYAISKLGPGKGYELHAATDTPPSVVHVHVCSDQENEEEMERMKRPKPKIIQTRRP 189
QY 191 EYTPHLS 198
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QY 4 VDLQDLP---SATIACHLDPRVFDGLCRAKFESLRTYDKDITTFQYFKSFKRVRINFSN 60
Db 1 MFDPRFSYFSSLIACVANDVDFSESETRAKFESLRTYDKDITTFQYFKSFKRVRINFSN 60
QY 61 PLSAADARLRLHKTEFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVGWKQV 120
Db 61 PLSAADARLRLHKTEFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVGWKQV 120
QY 121 EDATPVINYDLIYAIKLGPGKGYELHAATDTPPSVVHVHVCSDQENEEEMERMKRP 180
Db 121 EDATPVINYDLIYAIKLGPGKGYELHAATDTPPSVVHVHVCSDQENEEEMERMKRP 180
QY 181 KPQIOTRRPEYTPHLS 198
Db 181 KPQIOTRRPEYTPHLS 198

RESULT 10
US-09-782-953-13
; Sequence 13, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSD:674PZ1
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
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Db 190 EYTPHLS 197
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Db 111 ARARIELHETQPRGKKLYFAQVQPTDGDGKLHLAPPQAKQFLISPPSSPPVGWQPI 170
|||||
QY 121 EDATPVINYDLYAISKLGEGKVELHAATDPTSPVVHVHVCSDQNEEEEEEMERKRP 180
|||||
Db 171 NDATPVINYDLYAVAKLGEGKVELHAGTSTPSPVVHVHVCSDIEBEDPK-----TSP 225
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QY 181 KPRIIOTRRPEYTP 194
|||||
Db 226 KPRIIOTRRPGLPP 239
|||||

RESULT 14
US-10-290-438-2
; Sequence 2, Application US/10290438
; Publication No. US20030186333A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEIN
; FILE REFERENCE: FC-0013-ICIP
; CURRENT APPLICATION NUMBER: US/10/290,438
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 09/614,474
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030186333A1 247500.5
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 11
; OTHER INFORMATION: unknown or other
US-10-290-438-2

Query Match 59.2%; Score 620.5; DB 14; Length 255;
Best Local Similarity 62.4%; Pred. No. 1.1e-53;
Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;

QY 5 DLQDLPSTAIACHLDRPVFDGLCRAKFESLFTYDKDTTFQYFKSKRVIRNFSNPLSA 64
|||||
Db 63 DFNDLPNSLPACNVHQSVEGEEKFGLPRTYDDCVTFQLFKSFRRVIRNFSNPKSA 122
|||||
QY 65 ADARLRLHKTFLGKEMKLYFAQTLHGSS-----HLAPPNDKQFLISPPASPPVGWQV 120
|||||
Db 123 ARARIELHETQPRGKKLYFAQVQPTDGDGKLHLAPPQAKQFLISPPSSPPVGWQPI 182
|||||
QY 121 EDATPVINYDLYAISKLGEGKVELHAATDPTSPVVHVHVCSDQNEEEEEEMERKRP 180
|||||
Db 183 NDATPVINYDLYAVAKLGEGKVELHAGTSTPSPVVHVHVCSDIEBEDPK-----TSP 237
|||||
QY 181 KPRIIOTRRPEYTP 194
|||||
Db 238 KPRIIOTRRPGLPP 251
|||||

RESULT 15
US-09-782-953-9
; Sequence 9, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSD:674P21
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; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-782-953-9

Query Match      58.5%; Score 613.5; DB 9; Length 197;
Best Local Similarity 63.3%; Pred. No. 4e-53;
Matches 119; Conservative 22; Mismatches 38; Indels 9; Gaps 2;

QY      11 SATIACHLDPRVFDGLCRAKPESLFTYDKOTTFOYFKSFKRVIRINFNSPLSAADARLR 70
DB      11 STLIVACVVDVEVTNQEVKEFGLFRTYDECVTFQLFKSFRRVRINFSHPKSAARARIE 70

QY      71 LHKTEFLGKEMKLYFAQTLHIGSS----HLAPNPDKQFLISPPASPPVGVWKQVEDATEV 126
DB      71 LHETQFRGKKLYFAQVOTPETDGDKHLAPQPAKQFLISPPSSPPVGVWKPFISDATEV 130

QY      127 INVDLLYAIKLGPGKYLHAATDPTPSVVHVCSDOENEEEEEMERMKRPKPKIIQ 186
DB      131 LNYDLLYAVAKLGPGEKYLHAGTESTPSVVHVCDSDMEEBEDPK-----TSPKPKIIQ 185

QY      187 TRRPEYTP 194
DB      186 TRRPGGLPP 193
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Search completed: November 16, 2005, 16:53:28
Job time : 101.8 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:43:46 ; Search time 12.15 Seconds
(without alignments)
1567.977 Million cell updates/sec

Title: US-09-575-580B-4
Perfect score: 1048
Sequence: 1 MEEVDLQDLPSATIACHLDP.....RPKPKLIQTRPEYTPIHLS 198

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	355	33.9	239	T34305	hypothetical prote
2	139.5	13.3	315	T49641	nebula related pro
3	95.5	9.1	163	S62444	conserved hypothet
4	94	9.0	318	C84651	hypothetical prote
5	92	8.8	992	T46337	hypothetical prote
6	91.5	8.7	1274	D84485	probable retroelem
7	88	8.4	284	B48316	surfactant protein
8	88	8.4	630	S29796	hypothetical prote
9	88	8.4	721	S29795	hypothetical prote
10	86.5	8.3	822	S30198	Na+/H+-exchanging
11	86	8.2	338	S73902	UDP-glucose 4-epim
12	84.5	8.1	719	S51739	transcription repr
13	83	7.9	561	JC2436	5'-nucleotidase [E
14	83	7.9	1173	T31421	C-terminal domain-
15	82	7.8	697	E96752	hypothetical prote
16	82	7.8	1477	T13797	tumor suppressor pr
17	81.5	7.8	528	C69323	conserved hypothet
18	81	7.7	151	T10768	latex allergen Hev
19	80.5	7.7	280	C64471	hypothetical prote
20	80.5	7.7	360	S12850	protein TPX - Ther
21	80	7.6	681	T17342	hypothetical prote
22	79.5	7.6	797	A70453	glutamate ammonia
23	79.5	7.6	904	I38757	homolog of Drosoph
24	79.5	7.6	926	I38756	hypothetical prote
25	79.5	7.6	1020	B86414	hypothetical prote
26	79.5	7.6	1136	T26953	hypothetical prote
27	79.5	7.6	1146	C83304	hypothetical prote
28	79.5	7.6	1557	T29132	hypothetical prote
29	79	7.5	684	F85075	hypothetical prote

30	79	7.5	1154	2	A39577	protein-tyrosine k
31	79	7.5	1216	2	T09224	spindle assembly c
32	79	7.5	13055	2	T16580	hypothetical prote
33	78.5	7.5	211	2	S37792	hypothetical prote
34	78.5	7.5	290	2	T42526	hypothetical prote
35	78.5	7.5	1706	2	I84499	zinc finger protei
36	78.5	7.5	1880	2	T18531	tractin - medicina
37	78	7.4	454	2	AE1244	acetyl-CoA coxsy
38	78	7.4	467	1	A49377	involucrin - mouse
39	78	7.4	677	2	T00369	hypothetical prote
40	77.5	7.4	441	2	A86151	hypothetical prote
41	77.5	7.4	455	2	B86427	hypothetical prote
42	77.5	7.4	621	2	T15929	hypothetical prote
43	77.5	7.4	627	2	A41609	dnak-type molecula
44	77.5	7.4	1211	2	T42230	AF4 protein - mous
45	77	7.3	340	2	B84771	hypothetical prote

ALIGNMENTS

RESULT 1

T34305
hypothetical protein F54E7.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34305
R:Bentley, D.
submitted to the EMBL Data Library, June 1994
A:Description: The sequence of C. elegans cosmid F54E7.
A:Reference number: Z21502
A:Accession: T34305
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-239 <BEN>
A:Cross-references: UNIPROT:P53806; EMBL:U00067; PIDN:AAC77519.1; GSPDB:GN00021; CESP:F54E7
A:Experimental source: strain Bristol N2; clone F54E7
C:Genetics:
A:Gene: CESP:F54E7.7
A:Map position: 3
A:Introns: 40/3; 78/2; 165/2; 205/1

Query Match	33.9%	Score 355;	DB 2;	Length 239;		
Best Local Similarity	41.0%;	Pred. No. 3.9e-24;				
Matches 75;	Conservative 36;	Mismatches 68;	Indels 4;	Gaps 3;		
QY	8	DLPSATIACHLDP	RVFDGLCRAPESL	PTDYDKDTTQYFKSFKRVR	INFSNPLSAADA	67
Db	27	DLFNAIIIVQVPED	VFDNKQDKANFSS	LFTQIEKDIHDFLRSFRVR	VIFSSPENATAA	86
QY	68	RLRLHKTEFLGKEM	KLYFAQTLHI--GSSH	LAPPNPDKQFLISPPAS	PPVGNKQVEDATP	125
Db	87	KLIQVGFSGKHELK	AKFAQRIYMSANSQ	MLSPPLKQFLISPPCS	PPVGMETKDMPP	146
QY	126	VT--NYDLLVAIK	GLGPKGEYELHAAT	PTDPTPVSVHVCS	DQNEEEEMERKRPKI	184
Db	147	VVCNFDLMARLAS	FAIDEXEYVHGDEL	TPAIIIVHPCETPID--	VPSAIEMPTRPSSPS	205
QY	185	IQT	187			
Db	206	LQS	208			

RESULT 2

T49641
nebula related protein [imported] - Neurospora crassa
N:Alternate names: protein B5022.230
C:Species: Neurospora crassa
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022

Db 301 EQAPSPAAACEKGEHQSAEELGPGQEAEDPEEKVAVSPTPPVSPVSTRSTPVPAPPEQ 360
QY 157 -----VVHYCESDQNEEEEMERMKPKKIQTRRPEYTPIH 196
Db 361 LSEAALKAMEEAAVAQVLEQDORHLLSKQ-EKKOQLREKLQCQEEIEILRH 411

RESULT 6
D84485
probable retroelement pol polyprotein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: D84485
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84485
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-1274 <STO>
A;Cross-references: UNIPROT:Q9ZQK2; GB:AE002093; NID:94309763; PIDN:AAD15532.1; GSPDB:GN
C;Genetics:
A;Gene: At2g07400
A;Map position: 2

Query Match 8.7%; Score 91.5; DB 2; Length 1274;
Best Local Similarity 23.1%; Pred. No. 7.8;
Matches 51; Conservative 30; Mismatches 83; Indels 51; Gaps 9;
QY 24 VDGLCRAKFESLFRDYDKDTTFQYFKSKVRINFSNPLSAADAR-LRLHKTEFLGKE-- 80
Db 673 IESRVAKTEGRFGSTENDV-----KQIKELKAIADSKSSVIRMYLAKTQPTQQDN 727
QY 81 MKLYFAQTLLHI-----GSSHLAPPNP-----KQFLISPPA-----SPVGVWK 118
Db 728 PKVOTQOTPDVPKPTNNQFATSPPPSKQADVGVKKEKTLNELIQPPGRRGRKPSQPK 787
QY 119 QVEDATPVNYDLYIAIKLGPGEKYLHA-----ATDTPSPVVHVHVCSDQNEEEEEE 173
Db 788 KVSPTMPKI-----TIKKLKPSQEAKEABEDSDVDVDTDKVVSYNEMLPESDDEEE 841

QY 174 MERMKRPKPKIIOTR-----PEVTPIHLS 198
Db 842 TERLKSVEIRLTKVLKPDGRSLINPEAMPHTS 876

RESULT 7
B48516
surfactant protein A receptor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-Apr-1994
C:Accession: B48516
R;Strayer, D.S.; Yang, S.; Jerng, H.H.
J. Biol. Chem. 268, 18679-18684, 1993
A;Title: Surfactant protein A-binding proteins. Characterization and structures.
A;Reference number: A48516; MUID:93366778; PMID:8360162
A;Accession: B48516
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A;Residues: 1-284 <STR>
A;Cross-references: GB:L10124

Query Match 8.4%; Score 88; DB 2; Length 284;
Best Local Similarity 24.1%; Pred. No. 2.5;
Matches 40; Conservative 24; Mismatches 62; Indels 40; Gaps 7;
QY 27 LCAKAFESLFRDYDKDTTFQYFKSKVRINFSNPLSAADARLRLHKTEFLGKEMKLYFA 86
Db 3 MCYGMGSLFRSGSRQTLFA-----SQVMRYAD-----LYAAGFIN---LLYYP 43

QY 87 QTLHIGSSHLAPPNP-----DKQFLISPPAS-----PPVGWKQVEDATPVINYDLYAI 135
Db 44 FSVLPFAAHVLMHSTVEHTHVDINEMESPLATNRRTSVDFPKD-----TDYKRHQLTRSI 99
QY 136 SKLGPGEKYLHAADTPTSPVVHVHVCSDQNEEEEMERMKRPK 181
Db 100 SEIKPPNLFPL-----APQETHCHDEDDDEEEEBECCGKPK 139

RESULT 8
S29796
hypothetical protein 2280 - evening primrose chloroplast (fragment)
C:Species: chloroplast Oenothera villaricae (evening primrose)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S29796; S19986
R;Nimzyk, R.; Schoendorf, T.; Hachtel, W.
Curr. Genet. 23, 265-270, 1993
A;Title: In-frame length mutations associated with short tandem repeats are located in
A;Reference number: S29795; MUID:93169690; PMID:8435856
A;Accession: S29796
A:Molecule type: DNA
A;Residues: 1-630 <NIM>
A;Cross-references: UNIPROT:P31569; EMBL:X64615; NID:gl4331; PID:gl4332
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 8.4%; Score 88; DB 2; Length 630;
Best Local Similarity 26.2%; Pred. No. 6.7;
Matches 45; Conservative 23; Mismatches 48; Indels 56; Gaps 10;
QY 16 CHLDP-RVFV-DGLCRAKFESLFRDYDKDTTFQYFKSKVRINFSNPLSAADARLRLHK 73
Db 81 CSIDPISIVIKKNCAGDSSLVKWY-----FELGTSMKKLT----- 118
QY 74 TFLGKEMKLYFAQTLLHIGS-----SHLAPPNDKQFLISPPASPPVGWKQVEDATPVINYD 130
Db 119 -----LLYLLTCSAGSIAQDLLSPGPDQNLIT-----SYGLVEN-----DSD 157
QY 131 LLVATSLKGPGEKYLHAA-----TDTPSPVVHVHVCSDQNEEE-----EEME 175
Db 158 LVHGLSDIVHG--LLELGALVGSSPTTEEVGTEEGTEEGTEEGTEEGTE 208

RESULT 9
S29795
hypothetical protein 2280 - evening primrose (Oenothera picensis subsp. picensis) chlor
C:Species: chloroplast Oenothera picensis subsp. picensis (evening primrose)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S29795; S19983
R;Nimzyk, R.; Schoendorf, T.; Hachtel, W.
Curr. Genet. 23, 265-270, 1993
A;Title: In-frame length mutations associated with short tandem repeats are located in
A;Reference number: S29795; MUID:93169690; PMID:8435856
A;Accession: S29795
A:Molecule type: DNA
A;Residues: 1-721 <NIM>
A;Cross-references: UNIPROT:P31568; EMBL:X64616; NID:gl4334; PID:gl4335
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 8.4%; Score 88; DB 2; Length 721;
Best Local Similarity 26.2%; Pred. No. 7.9;
Matches 45; Conservative 23; Mismatches 48; Indels 56; Gaps 10;
QY 16 CHLDP-RVFV-DGLCRAKFESLFRDYDKDTTFQYFKSKVRINFSNPLSAADARLRLHK 73
Db 81 CSIDPISIVIKKNCAGDSSLVKWY-----FELGTSMKKLT----- 118
QY 74 TFLGKEMKLYFAQTLLHIGS-----SHLAPPNDKQFLISPPASPPVGWKQVEDATPVINYD 130
Db 119 -----LLYLLTCSAGSIAQDLLSPGPDQNLIT-----SYGLVEN-----DSD 157

S73902 UDP-glucose 4-epimerase gALE - Mycoplasma pneumoniae (strain ATCC 29342)
N;Alternate names: hypothetical protein A65_orf338
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S73902
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73902
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-338 <HM>
A;Cross-references: UNIPROT: P75517; EMBL: AE000056; GB: U00089; NID: g1674263; PIDN: AAB9622
A;Note: The nucleotide sequence was submitted to the EMBL Data Library, November 1996
C;Genetics:
A;Gene: galE
A;Genetic code: SGC3
C;Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
F;8-338/Domain: UDPglucose 4-epimerase homology <UDP>

Query Match 8.2%; Score 86; DB 2; Length 338;
Best Local Similarity 27.9%; Pred. No. 4.7;
Matches 34; Conservative 19; Mismatches 59; Indels 10; Gaps 3;

QY 4 VLDQLPSATIACHLDPRV----FVDGLCRAKFESLFRTYDKDTTFQYKFSKRVIRNFS 59
| | : : : | | : : : | : : : | : : : | : : : | : : : | : : : |

QY 45 FOYFKSKVRINFSNPLSAADARLRHLKTEFLGKEMKLYFAOTLHIGSSHLAPPNP--- 101
DB 450 FASOMRYAD---LYAASFN---LLYPPSYLFRAAHVLMPHSTV 490
QY 102 -----DKQFLISPPAS---PPVGKQVEDATPVINYDLVLAISKLGPGEKYELHAATDPT 153
DB 491 EHTHVDINEMESPLATNRTSVDFKD---TDYKRHLQTRISIEIKPPNLFPL-----A 540
QY 154 PSVVVHVHVCSDQENEEEEEEME 175
DB 541 PQEITH-CHDEDDDEEEEEE 561
RESULT 14
T31421
C-terminal domain-binding protein ral - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31421
R:Yuryev, A.; Patturajan, M.; Litingtung, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord
Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996
A:Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts with
A:Reference number: Z21024; MUID:96293459; PMID:8692929
A:Accession: T31421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1173 <YUR>
A:Cross-references: UNIPROT:Q63624; EMBL:U49056; NID:gl438531; PID:gl438532; PIDN:AAC526
A:Experimental source: hippocampus

Query Match 7.9%; Score 83; DB 2; Length 1173;
Best Local Similarity 24.1%; Pred. No. 40;
Matches 49; Conservative 19; Mismatches 88; Indels 48; Gaps 7;
QY 1 MEEVDLQDLPSATIACHLD--PRFVVDGLCRKPFESLFTYDKDTTFQYFKSKVRINRF 58
DB 14 VEVVSILDPDPTWVPSHLDPQSESDVL--ELVAEVRIGDRDP-----M 56
QY 59 SNPLSAADARLRHLKTEFLGKEMK-----LYFAOTLHIGSSHLAPP-----N 100
DB 57 PLFVPSLLPLRLAWRT---GKTVSPQSHASRRACSRHLLTLGTGCGGAPPAPPPSSGSS 113
QY 101 PDKQFLISPPASPPVGKQVEDATPVINYDLVLAISKI-----GPGEKYELHAATDP 152
DB 114 PPSPPSSSPSPPP 173
QY 153 TPSVVHVHVCSDQENEEEEEEME 175
DB 174 NPSSSGTGPSPSEEEEEEEE 196

RESULT 15
E96752
hypothetical protein F28P22.5 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E96752
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96752
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-697 <STO>

A:Cross-references: UNIPROT:Q9CAI9; GB:AE005173; NID:g6648152; PIDN:AAF21152.1; GSPDB:G
C:Genetics:
A:Gene: F28P22.5
A:Map position: 1

Query Match 7.8%; Score 82; DB 2; Length 697;
Best Local Similarity 24.7%; Pred. No. 26;
Matches 44; Conservative 23; Mismatches 65; Indels 46; Gaps 7;

QY 40 DKDTTQYFKS-----FKVRIRINPSNPLS-----AADARLRHLKTEFLGKEMK 82
DB 291 DKDTTNQKENSQETPMSDEKIELPRALSRETOKTQSAAFQAAEIAKRIAKME--SQKRR 348
QY 83 LYFAOTLHIGSSHLAPPNPKQFLISPPASPPVGKQVEDATPVINYDLVLAIS---KL 139
DB 349 LLEMQA-----NLDKQMMFTTVSYRRYSIKQVEDAT-----YGFSDALKIG 389
QY 140 PGKEYELHAATDPTPSVVHVHVCSD-----QENEEEEEEMERMKRPKPKIOTRRPEY 192
DB 390 EGGYGPVYKAVLDYTSVAIKILKSGITGLKQFQOEIVLSSMRHPNMVILLGACPEY 447

Search completed: November 16, 2005, 17:13:06
Job time : 14.15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:32:05 ; Search time 49.5 Seconds
(without alignments)
2048.317 Million cell updates/sec

Title: US-09-575-580B-4

Perfect score: 1048

Sequence: 1 MBEVDLIQPLSATIACHLDP.....RPKPKIIQRRPEYTPIHLS 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_treml.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1040	99.2	198	1 CCPI_MOUSE	Q9jhg6 mus musculus
2	1040	99.2	251	2 Q7TNY3	Q7tny3 mus musculus
3	1002.5	95.7	197	1 CCPI_HUMAN	P53805 homo sapien
4	1002.5	95.7	252	2 Q7Z555	Q7Z555 homo sapien
5	887.5	84.7	199	2 Q8K4S2	Q8K4S2 cricetus
6	884.5	84.4	197	1 CCPI_CRIGR	O35847 cricetus
7	883.5	84.3	197	2 Q6XXM7	O6xxm7 ovis aries
8	883.5	84.3	199	2 Q6IN33	Q6in33 rattus norv
9	847.5	80.9	242	2 Q6ZMM3	Q6zmm3 homo sapien
10	834.5	79.6	231	2 Q7ZXP4	Q7zxp4 xenopus lae
11	784.5	74.9	199	2 Q6DK90	Q6dk90 xenopus tro
12	777.5	74.2	199	2 Q7T0U1	Q7t0u1 xenopus lae
13	643.5	61.4	196	2 Q6DGB1	Q6dgb1 brachydanio
14	639.5	61.0	210	2 Q6DC33	Q6dc33 brachydanio
15	627.5	59.9	243	2 Q8VIP4	Q8vip4 mus musculus
16	622.5	59.4	243	2 Q8CH26	Q8ch26 rattus norv
17	618.5	59.0	230	2 Q6DC39	Q6dc39 brachydanio
18	613.5	58.5	197	1 CCP2_MOUSE	Q9jhg2 mus musculus
19	609.5	58.2	225	2 Q86YJ0	Q86yj0 homo sapien
20	608.5	58.1	192	2 Q8VIP5	Q8vip5 mus musculus
21	608.5	58.1	197	2 Q8CH27	Q8ch27 rattus norv
22	607.5	58.0	243	2 Q8N116	Q8n116 homo sapien
23	606.5	57.9	195	2 Q6NSN4	Q6nsn4 brachydanio
24	597	57.0	239	1 CCP3_MOUSE	Q9jkk0 mus musculus
25	596.5	56.9	197	1 CCP2_HUMAN	Q14206 homo sapien
26	596	56.9	241	1 CCP3_HUMAN	Q9uka8 homo sapien
27	379.5	36.2	292	1 SRA_DROME	Q9x2l8 drosophila
28	351	33.5	207	1 CCPI_CAEAL	P53806 caenorhabdi
29	155	14.8	29	2 Q9HZAI	Q9hza1 homo sapien
30	139.5	13.3	315	2 Q9P5S9	Q9p5s9 neurospora
31	115.5	11.0	249	2 Q66PG0	Q66pg0 cryptococcus

32	114.5	10.9	249	2	Q9P4A1	Q9p4a1 cryptococcus
33	114.5	10.9	405	2	Q86JH9	Q86jh9 dictyosteli
34	106.5	10.2	264	2	Q6G6F1	Q6g6f1 yarrowia li
35	102	9.7	775	2	Q7SAZ0	Q7saz0 neurospora
36	95.5	9.1	163	1	YA9F_SCHPO	Q09791 schizosacch
37	94	9.0	318	2	Q8LFB4	Q8lfb4 arabidopsis
38	94	9.0	318	2	Q8VZ43	Q8vz43 arabidopsis
39	94	9.0	318	2	Q8SL96	Q8sl96 arabidopsis
40	93	8.9	227	2	Q6YX04	Q6yx04 oryza sativ
41	93	8.9	513	2	Q8ALP8	Q8alp8 bacteroides
42	92	8.8	328	2	Q9LSD3	Q9lsd3 arabidopsis
43	92	8.8	513	2	Q64ZB5	Q64zb5 bacteroides
44	92	8.8	992	2	Q9NTH6	Q9nth6 homo sapien
45	92	8.8	1456	2	Q9UPV0	Q9upv0 homo sapien

ALIGNMENTS

RESULT 1

CCPI_MOUSE STANDARD: PRT: 198 AA.
ID CCPI_MOUSE Q9JWQ4; Q9JKS0; Q9JK51; Q9JKK2; Q9JKK3;
AC Q9JHG6; Q9LWQ4; Q9JKS0; Q9JK51; Q9JKK2; Q9JKK3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcipressin 1 (Down syndrome critical region protein 1 homolog)
DE (Myocyte-enriched calcineurin interacting protein 1) (MCIP1).
GN Names=Dscr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A. (ISOFORM A).
RC STRAIN=BALB/C; TISSUE=Brain;
RX MEDLINE=20534792; PubMed=11080588; DOI=10.1016/S0378-1119(00)00407-8;
RA Strippoli P., Petrini M., Lenzi L., Carinci P., Zannotti M.;
RT "The murine DSCR1-like (Down syndrome candidate region 1) gene family:
RT conserved synteny with the human orthologous genes.";
RL Gene 257:223-232(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=20187590; PubMed=10722714; DOI=10.1074/jbc.275.12.8719;
RA Rothmel B., Vega R.B., Yang J., Wu H., Baesel-Duby R.,
RA Williams R.S.;
RT "A protein encoded within the Down syndrome critical region is
RT enriched in striated muscles and inhibits calcineurin signaling.";
RL J. Biol. Chem. 275:8719-8725(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM A), AND FUNCTION.
RC TISSUE=Fetal brain;
RX MEDLINE=21152320; PubMed=11231093; DOI=10.1016/S0925-4773(00)00583-9;
RA Casas C., Martinez S., Pritchard M.A., Fuentes J.J., Nadal M.,
RA Guinera J., Arbones M., Florez J., Soriano E., Estivill X.,
RA Alcantara S.;
RT "Dscr1, a novel endogenous inhibitor of calcineurin signaling, is
RT expressed in the primitive ventricle of the heart and during
RT neurogenesis.";
RL Mech. Dev. 101:289-292(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C).
RX Fuentes J.J., Pritchard M.A., Pucharcos C., Estivill X.;
RT "Down syndrome candidate region 1 (Dscr1), one of three alternatively
RT spliced exon 1 transcripts.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM C).
RC STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,


```
Query Match 99.2%; Score 1040; DB 2; Length 251;
Best Local Similarity 99.5%; Pred. No. 1.2e-80;
Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEEVDLQDLPSATIACHLDRPVVDGLCRAKFSLRTYDKDTTFQYFKSFKRVRINFNSN 60
DB 54 MEEVDLQDLPSATIACHLDRPVVDGLCRAKFSLRTYDKDTTFQYFKSFKRVRINFNSN 113

QY 61 PLSAADARLRHLKTEFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVCGKQV 120
DB 114 PLSAADARLRHLKTEFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVCGKQV 173

QY 121 EDATPVINYDLYLAISKLGPEKGYELHAATDTPPSVVHVHVCSDQNEEBEEMERMKRP 180
DB 174 EDATPVINYDLYLAISKLGPEKGYELHAATDTPPSVVHVHVCSDQNEEBEEMERMKRP 233

QY 181 KPKIIOTRRPEYTPIHLS 198
DB 234 KPKIIOTRRPEYTPIHLS 251

RESULT 3
CCPI_HUMAN STANDARD; PRT; 197 AA.
AC P53805; O00582; O00583; Q96R03; Q9BU69; Q9UF15; Q9UME4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcipressin 1 (Down syndrome critical region protein 1) (Myocyte-
enriched calcineurin interacting protein 1) (MCIP1) (Adapt78).
GN Name=DSCR1; Synonyms=ADAPT78, DSCR1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
RX MEDLINE=96121593; PubMed=8595418;
RA Fuentes J.-J., Pritchard M.A., Planas A.M., Bosch A., Ferrer I.,
RA Estivill X.;
RT "A new human gene from the Down syndrome critical region encodes a
RT proline-rich protein highly expressed in fetal brain and heart.";
RL Hum. Mol. Genet. 4:1935-1944(1995).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=97468152; PubMed=9325060; DOI=10.1006/geno.1997.4866;
RA Fuentes J.-J., Pritchard M.A., Estivill X.;
RT "Genomic organization, alternative splicing, and expression patterns
of the DSCR1 (Down syndrome candidate region 1) gene.";
RL Genomics 44:358-361(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Hua F., Wu J., Zhou Y., Zhang B., Peng X., Qiang B., Yuan J.,
RA Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=bung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1-164 FROM N.A. (ISOFORM 2).
RC TISSUE=Breast;
RA Crawford D.R., Leahy K.P., Davies K.J.A.;
RT "Adapt78, a calcium and oxidant-inducible RNA.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP CHARACTERIZATION.
RX MEDLINE=20320698; PubMed=10861295; DOI=10.1093/hmg/9.11.1681;
RA Fuentes J.-J., Genesca L., Kingebury T.J., Cunningham K.W.,
RA Perez-Riba M., Estivill X., de la Luna S.;
RT "DSCR1, overexpressed in Down syndrome, is an inhibitor of
calcineurin-mediated signaling pathways.";
RL Hum. Mol. Genet. 9:1681-1690(2000).
CC -!- FUNCTION: Inhibits calcineurin-dependent transcriptional responses
by binding to the catalytic domain of calcineurin A. Could play a
role during central nervous system development.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=P53805-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P53805-2; Sequence=VSP_001314;
CC Name=3;
CC IsoId=P53805-3; Sequence=VSP_001315;
CC Name=4;
CC IsoId=P53805-4; Sequence=VSP_001316;
CC -!- TISSUE SPECIFICITY: Highly expressed heart, brain and skeletal
muscle. Also expressed in all other tissues.
CC -!- INDUCTION: By calcium.
CC -!- SIMILARITY: Belongs to the DSCR1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
CC
CC EMBL; U28833; AAB81557.1; -
CC EMBL; U85265; AAB84370.1; -
CC EMBL; U85266; AAB84371.2; -
CC EMBL; U85267; AAB84372.1; -
CC EMBL; AF400423; AAK92478.1; -
CC EMBL; BC002864; AAO02864.1; -
CC EMBL; U53821; AAF21218.1; -
CC Genew; HGNC:3040; DSCR1.
CC H-InvDB; HIX0016091; -
CC MIM; 602917; -
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0003700; F:transcription factor activity; TAS.
CC GO; GO:0007417; P:central nervous system development; TAS.
CC GO; GO:0008015; P:circulation; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR006931; Calcipressin.
CC Pfam; PF04847; Calcipressin; 1.
CC Alternative splicing.
CC DOMAIN 156 174
CC VARSPLIC 1 28
CC
CC VARSPLIC 1 29
CC
CC VARSPLIC 1 80
CC
CC
```

FT CONFLICT 147 147 H -> R (in Ref. 3).
 FT CONFLICT 159 159 H -> Q (in Ref. 5).
 SQ SEQUENCE 197 AA; 22637 MW; 1BD426BB88167B6C CRC64;

Query Match 95.7%; Score 1002.5; DB 1; Length 197;
 Best Local Similarity 96.5%; Pred. No. 1.4e-77;
 Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MBEVDLQDLPSATIACHLDPVFDGLCRKAFESLFRITYDKDTTFQYFKSFRRVINFNSN 60
 DB 1 MBEVDLQDLPSATIACHLDPVFDGLCRKAFESLFRITYDKDTTFQYFKSFRRVINFNSN 60
 QY 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQV 120
 DB 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQV 120
 QY 121 EDATPVINDLLVAISKLGPGKGYELHAATDTPSVVHVHVCSDQDNNEEEMERMKRP 180
 DB 121 EDATPVINDLLVAISKLGPGKGYELHAATDTPSVVHVHVCSDQDNNEEEMERMKRP 179
 QY 181 KPKIOTRRPEYTPIHLS 198
 DB 180 KPKIOTRRPEYTPIHLS 197

RESULT 4
 QY2555 PRELIMINARY; PRT; 252 AA.
 AC Q72555;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Calcipressin 1 large isoform.
 GN Name=DSCR1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=22806131; PubMed=12809556; DOI=10.1042/BJ20030267;
 RA Genesca L., Aubareda A., Fuentes J.J., Estivill X., de la Luna S.,
 RA Perez-Riba M.;
 RT "Phosphorylation of calcipressin 1 increases its ability to inhibit
 RT calcineurin and decreases calcipressin half-life.";
 RL Biochem. J. 374:567-575(2003).
 DR EMBL; AV325903; AAP96743.1; -;
 DR GO; GO:0019722; P:calcium-mediated signaling; IEA.
 DR InterPro; IPR006931; Calcipressin.
 DR Pfam; PF04847; Calcipressin; 1.
 SQ SEQUENCE 252 AA; 28078 MW; 0B17133D03BD7AFA CRC64;

Query Match 95.7%; Score 1002.5; DB 2; Length 252;
 Best Local Similarity 96.5%; Pred. No. 1.9e-77;
 Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 MBEVDLQDLPSATIACHLDPVFDGLCRKAFESLFRITYDKDTTFQYFKSFRRVINFNSN 60
 DB 56 MBEVDLQDLPSATIACHLDPVFDGLCRKAFESLFRITYDKDTTFQYFKSFRRVINFNSN 115
 QY 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQV 120
 DB 116 PLSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQV 175
 QY 121 EDATPVINDLLVAISKLGPGKGYELHAATDTPSVVHVHVCSDQDNNEEEMERMKRP 180
 DB 176 EDATPVINDLLVAISKLGPGKGYELHAATDTPSVVHVHVCSDQDNNEEEMERMKRP 234
 QY 181 KPKIOTRRPEYTPIHLS 198
 DB 235 KPKIOTRRPEYTPIHLS 252

RESULT 5
 QYK4S2 PRELIMINARY; PRT; 199 AA.
 AC QYK4S2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myocyte-enriched calcineurin-interacting protein 1.
 GN Name=mcip 1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Odashima M., Nagata K., Obata K., Somura F., Izawa H., Miyazaki T.,
 RA Murata Y., Seo H., Yamada Y., Yokota M.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB075973; BAC06443.1; -;
 DR GO; GO:0019722; P:calcium-mediated signaling; IEA.
 DR InterPro; IPR006931; Calcipressin.
 DR Pfam; PF04847; Calcipressin; 1.
 SQ SEQUENCE 199 AA; 22976 MW; 94A311E66D59F0B9 CRC64;

Query Match 84.7%; Score 887.5; DB 2; Length 199;
 Best Local Similarity 91.5%; Pred. No. 9e-68;
 Matches 173; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 11 SATIACHLDPVFDGLCRKAFESLFRITYDKDTTFQYFKSFRRVINFNSPLSAADARLR 70
 DB 11 SSLIACVANGDVFSSETRAKFESLFRITYDKDTTFQYFKSFRRVINFNSPLSAADARLR 70
 QY 71 LHKTEFLGKEMKLYPAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQVEDATPVIND 130
 DB 71 LHKTEFLGKEMKLYPAQTLHGSSHLAPPNDPKQFLISPPASPPVGVKQVEDATPVIND 130
 QY 131 LLYAISKLGPGKGYELHAATDTPSVVHVHVCSDQ-ENEEEEEEMERMKRPKPKIIQTRR 189
 DB 131 LLYAISKLGPGKGYELHAATDTPSVVHVHVCSDQEEEEEEMERMKRPKPKIIQTRR 190
 QY 190 PEYTPIHLS 198
 DB 191 PEYTPIHLS 199

RESULT 6
 CCPI_CRIGR STANDARD; PRT; 197 AA.
 ID CCPI_CRIGR
 AC O35847;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Calcipressin 1 (Down syndrome critical region protein 1 homolog)
 DE (Oxidative-induced protein Adapt78).
 GN Name=DSCR1; Synonyms=ADAPT78;
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97329095; PubMed=9185608; DOI=10.1006/abbi.1997.0109;
 RA Crawford D.R., Leahy K.P., Abramova N., Lan L., Wang Y., Davies K.J.;
 RA "Hamster adapt78 mRNA is a Down syndrome critical region homologue
 RT that is inducible by oxidative stress.";
 RL Arch. Biochem. Biophys. 342:6-12(1997).
 CC -!- FUNCTION: Inhibits calcineurin-dependent transcriptional responses
 CC by binding to the catalytic domain of calcineurin A. Could play a
 CC role during central nervous system development (By similarity).
 CC -!- INDUCTION: By oxidative stress.
 CC -!- SIMILARITY: Belongs to the DSCR1 family.


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Db 191 PEYTPHLS 199
RESULT 9
Q62MW3 PRELIMINARY; PRT; 242 AA.
AC Q62MW3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16823.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Negahari K., Masuho Y., Negai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK131569; BAD18702.1; -.
DR GO; GO:0019722; P:calcium-mediated signaling; IEA.
DR InterPro; IPR006931; Calciopressin.
DR Pfam; PF04847; Calciopressin; 1.
SQ SEQUENCE 242 AA; 27850 MW; 4888F4EAB303BA81 CRC64;

Query Match 80.9%; Score 847.5; DB 2; Length 242;
Best Local Similarity 83.2%; Pred. NO. 3e-64;
Matches 164; Conservative 12; Mismatches 14; Indels 7; Gaps 2;

QY 8 DLPSATIACHLDPRVFDGLC-----RAKFSLERTYDKDTTFQYFKSKVRINFSP 61
Db NIPEDLLSYPESSLPQRHCAFHRSKAKFSLERTYDKDTTFQYFKSKVRINFSP 106
QY 62 LSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGWKQV 121
Db FSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGWKQV 166
QY 122 DATPVINYDLLVAISKLGPGKLYELHAATDTPSVVVHVCSQDQNEEEEMERMRPK 181
Db DATPVINYDLLVAITKLGPGKLYELHAATDTPSVVVHVCSQDQ-KEBEEEMERMRPK 225
QY 182 PKLIOTRRPEYTPHLS 198
Db PKLIOTRRPEYTPHLS 242

RESULT 10
Q7ZXP4 PRELIMINARY; PRT; 231 AA.
AC Q7ZXP4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Decrl-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044332; AAH4332.1; -.
DR GO; GO:0019722; P:calcium-mediated signaling; IEA.
DR InterPro; IPR006931; Calciopressin.
DR Pfam; PF04847; Calciopressin; 1.
SQ SEQUENCE 231 AA; 25991 MW; 66604BEC26491826 CRC64;

Query Match 79.6%; Score 834.5; DB 2; Length 231;
Best Local Similarity 78.4%; Pred. NO. 3.6e-63;
Matches 156; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

QY 1 MEEVDLQDLPSATIACHLDPRVFDGLCRKAKFSLEFRYDKDTTFQYFKSKVRINFSP 60
Db MESIDRALPTALIGCSLEPSVFDGIYRTKPSLFKAYDKBATFOYFKSKVRINFSP 92
QY 61 PLSAADARLRLHKTFLGKEMKLYFAQTLHGSSHLAPPNDPKQFLISPPASPPVGWKQV 120
Db PISAFAEARLQHKSEFLGKELKLYFAQTLHGSPHAPPNPEKQFLISPPSSPPVGWKQK 152
QY 121 EDATPVINYDLLVAISKLGPGKLYELHAATDTPSVVVHVCSQDQNE-EBEEMERMRK 179
Db EDASPVINYDLLVAISKLGPGKLYELHAATDTPSVVVHVCSQDQNELEIEDEBDGMSK 212
QY 180 PKPIIOTRRPEYTPHLS 198
Db PKPIIOTRRPEYTPHLS 231

RESULT 11
Q6DK90 PRELIMINARY; PRT; 199 AA.
AC Q6DK90;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Decrl-prov protein.
GN Name=decrl-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:22:56 ; Search time 125.95 Seconds
(without alignments)
743.120 Million cell updates/sec

Title: US-09-575-580B-5

Perfect score: 1296

Sequence: 1 EFVDPVRPRVRLGQOASIP.....TSPKPKINQTRRGLPPFGH 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Genesecp1980s:*
- 2: Genesecp1990s:*
- 3: Genesecp2000s:*
- 4: Genesecp2001s:*
- 5: Genesecp2002s:*
- 6: Genesecp2003as:*
- 7: Genesecp2003bs:*
- 8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1129	87.1	234	4 AAB31788	Aab31788 Amino aci
2	1129	87.1	243	7 ADB64062	ADB64062 Human pro
3	1129	87.1	255	5 AAM50760	Aam50760 Human Dow
4	1129	87.1	255	7 ADE37339	Ade37339 Human Dow
5	882	68.1	197	5 AAE18913	Aae18913 Mouse MCI
6	861	66.4	197	6 ABO07172	Abo07172 Human p53
7	848	65.4	192	5 AAE18916	Aae18916 Human MCI
8	848	65.4	192	7 ADE37341	Ade37341 Human Dow
9	708.5	54.7	241	5 AAE18917	Aae18917 Human MCI
10	708.5	54.7	241	6 ABO07173	Abo07173 Human p53
11	708.5	54.7	241	7 ADE37342	Ade37342 Human Dow
12	676.5	52.2	212	5 AAE18918	Aae18918 Human MCI
13	648	50.0	252	7 ADB64738	ADB64738 Human pro
14	616	47.5	197	5 AAE18915	Aae18915 Human MCI
15	616	47.5	197	5 AAE18914	Aae18914 Human MCI
16	616	47.5	197	7 ADE25770	Ade25770 Human pro
17	616	47.5	197	8 ADRI4119	Adri4119 Human NF-
18	613.5	47.3	198	5 AAE18912	Aae18912 Mouse MCI
19	606.5	46.8	198	5 AAE18911	Aae18911 Human MCI
20	582	44.9	242	8 ADRI0481	Adri0481 Human pro
21	565	43.6	171	2 AAW73898	Aaw73898 Human Dow
22	418.5	32.3	292	4 ABB71467	Abb71467 Drosophila
23	312	24.1	111	3 AAG01768	Aag01768 Human sec
24	289	22.3	142	3 AAB58452	Aab58452 Lung canc
25	213	16.4	58	4 AAM15671	Aam15671 Peptide #

ALIGNMENTS

RESULT 1

AAB31788

ID AAB31788 standard; protein; 234 AA.

XX

XX AAB31788;

XX AC

XX 30-APR-2001 (first entry)

XX

XX Amino acid sequence of a human detoxification protein.

XX Human; detoxification protein; DEX; cancer; leukaemia; melanoma;

KW adenocarcinoma; autoimmune disorder; inflammatory disorder;

KW rheumatoid arthritis; asthma; atherosclerosis; autoimmune thyroiditis;

KW psoriasis; ulcerative colitis; infection; cell proliferative disorder;

KW actinic keratosis; arteriosclerosis; cirrhosis; hepatitis.

XX

XX Homo sapiens.

XX

XX Key Location/Qualifiers

FT Peptide 1..27 "signal peptide"

FT Modified-site 58

FT Modified-site 75 /note= "potential phosphorylation site"

FT Modified-site 87 /note= "potential phosphorylation site"

FT Modified-site 94 /note= "potential phosphorylation site"

FT Modified-site 130 /note= "potential glycosylation site"

FT Modified-site 204 /note= "potential phosphorylation site"

FT Modified-site 215 /note= "potential phosphorylation site"

FT Modified-site 223 /note= "potential phosphorylation site"

XX

XX WO200104305-A2.

XX

XX 18-JAN-2001.

XX

XX 06-JUL-2000; 2000WO-US018509.

XX

XX 07-JUL-1999; 99US-0142678P.

XX (INCY-) INCYTE GENOMICS INC.

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PI Tang YT, Yue H;
XX WPI; 2001-147193/15.
DR N-PSDB; AAF25338.
XX
XX New human detoxification protein and polynucleotide, useful for
PT diagnosis, prevention and treatment of autoimmune/inflammatory disorders
PT and cell proliferative disorders including cancer.
XX
XX Claim 1; Page 77; 79pp; English.
XX
XX The present sequence represents a human detoxification polypeptide
CC (DCTX). DCTX and its (ant)agonists are useful for preventing or treating
CC disorders associated with decreased or increased expression or activity
CC of DCTX. DCTX polypeptides are useful for screening compounds that
CC specifically binds to DCTX and for identifying (ant)agonists. Diseases
CC prevented, treated and diagnosed include cancers (e.g. leukaemia,
CC melanoma, adenocarcinoma, cancers of the brain, bone marrow, breast,
CC kidney, liver, pancreas, prostate and uterus), autoimmune/inflammatory
CC disorders (e.g. rheumatoid arthritis, asthma, atherosclerosis, autoimmune
CC thyroiditis, psoriasis and ulcerative colitis), bacterial, fungal,
CC parasitic infections and cell proliferative disorders (e.g. actinic
CC keratosis, arteriosclerosis, cirrhosis and hepatitis). Anti-DCTX
CC antibodies may be used as antagonists, as a targeting or delivery
CC mechanism for bringing pharmaceutical agents into contact with cells or
CC tissues expressing DCTX and for diagnosis of DCTX-related disorders
XX
XX Sequence 234 AA;
SQ
Query Match 87.1%; Score 1129; DB 4; Length 234;
Best Local Similarity 92.5%; Pred. No. 3.7e-111;
Matches 209; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 14 GQASIPEDGGFLFLCCIDRDWAVTQCFAEAFQALTFDPSLNSLFCNVHQSVPFEE 73
Db 5 GQGHVPEDGGFLFLCCIDRDWAVTQCFAEAFQALTFDNDLPNSLFCNVHQSVPFEE 64
QY 74 SKEKEGLFRITYDECVTQFQKSFRRVRINFSPKSAARARIELHETQFRGKKLPLYFAQ 133
Db 65 SKEKEGLFRITYDCVTQFQKSFRRVRINFSPKSAARARIELHETQFRGKKLPLYFAQ 124
QY 134 VQTPETDGDGLHAPPQPAKQFLISPPSSPSGKWPISDATPVLYNLYLAVAKLGPGEK 193
Db 125 VQTPETDGDGLHAPPQPAKQFLISPPSSPPVGMQPINDDATPVLYNLYLAVAKLGPGEK 184
QY 194 YELHAGTESTPSVVHVCDSDMEREDPKTSKPKNQTRRPLGP 239
Db 185 YELHAGTESTPSVVHVCDSDIEREDPKTSKPKNQTRRPLGP 230
RESULT 2
ADB64062
XX ADB64062 standard; protein; 243 AA.
XX
XX ADB64062;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human protein encoded by clone BRAWH20014590.
XX
XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;
KW transcription-related protein; osteoporosis; neurological disease;
KW cancer; tumour.
XX
XX Homo sapiens.
XX
XX EP1308459-A2.
XX
XX 07-MAY-2003.
XX
XX 28-MAR-2002; 2002EP-00007401.
XX

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PR 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX
XX (HELI-) HELIX RES INST.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Maeuho Y;
XX
XX WPI; 2003-450961/43.
DR N-PSDB; ADB62092.
DR
XX
XX New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
XX Claim 1; Page; 222pp; English.
XX
XX The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
XX
XX Sequence 243 AA;
SQ
Query Match 87.1%; Score 1129; DB 7; Length 243;
Best Local Similarity 92.5%; Pred. No. 3.9e-111;
Matches 209; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 14 GQASIPEDGGFLFLCCIDRDWAVTQCFAEAFQALTFDPSLNSLFCNVHQSVPFEE 73
Db 14 GQGHVPEDGGFLFLCCIDRDWAVTQCFAEAFQALTFDNDLPNSLFCNVHQSVPFEE 73
QY 74 SKEKEGLFRITYDECVTQFQKSFRRVRINFSPKSAARARIELHETQFRGKKLPLYFAQ 133
Db 74 SKEKEGLFRITYDCVTQFQKSFRRVRINFSPKSAARARIELHETQFRGKKLPLYFAQ 133
QY 134 VQTPETDGDGLHAPPQPAKQFLISPPSSPSGKWPISDATPVLYNLYLAVAKLGPGEK 193
Db 134 VQTPETDGDGLHAPPQPAKQFLISPPSSPPVGMQPINDDATPVLYNLYLAVAKLGPGEK 193
QY 194 YELHAGTESTPSVVHVCDSDMEREDPKTSKPKNQTRRPLGP 239
Db 194 YELHAGTESTPSVVHVCDSDIEREDPKTSKPKNQTRRPLGP 239
RESULT 3
AAM50760
ID AAM50760 standard; protein; 255 AA.
XX
XX AAM50760;
XX

```


DT 18-APR-2002 (first entry)
 XX Human Down syndrome critical region 1-like 1 protein.
 XX
 XX Down syndrome critical region 1-like 1; DSCR1L1 alpha; human;
 KW Down syndrome; Alzheimer's disease; dementia; transgenic;
 KW neuroprotective; nontropic; anticonvulsant; diagnosis; therapy.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 11 /note= "encoded by TNG"
 FT
 FT Domain 129..199
 FT /note= "nucleic acid-binding domain"
 FT Region 169..176
 FT /note= "ISPPXSPP box"
 XX
 XX WO200204513-A2.
 XX
 XX 17-JAN-2002.
 XX
 XX 11-JUL-2001; 2001WO-US021982.
 XX
 XX 11-JUL-2000; 2000US-00614474.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Loring JF, Tingley DW, Edwards CM, Streeter DG;
 XX WPI; 2002-164633/21.
 DR N-PSDB; ABA91457.
 XX
 XX Novel Down syndrome critical region 1-like 1 protein and nucleic acid
 PT encoding the protein useful for diagnosis and treatment of Alzheimer's
 PT disease, Down syndrome and other forms of dementia.
 XX
 XX Claim 1; Page 47-49; 54pp; English.
 XX
 XX The present sequence is that of novel Down syndrome critical region 1-
 CC like 1 protein (DSCR1L1 alpha). Northern analysis indicated expression of
 CC DSCR1L1 alpha in various libraries, with the highest abundance in tissues
 CC from the nervous system, including tissues associated with schizophrenia,
 CC Huntington's disease, epilepsy and amyotrophic lateral sclerosis. An
 CC absence of DSCR1L1 expression was observed in 7 of 8 libraries from
 CC subjects with Alzheimer's disease. A claimed method for detecting
 CC differential expression of a nucleic acid encoding DSCR1L1 alpha can be
 CC used to diagnose Down syndrome, Alzheimer's disease and other forms of
 CC dementia. The purified DSCR1L1 alpha protein, or a portion of it, can be
 CC used to identify ligands which specifically bind the protein, such as a
 CC DNA or RNA molecule, peptide nucleic acid, peptide, protein, mimetic,
 CC agonist, antagonist, antibody, immunoglobulin, inhibitor or drug, for use
 CC as a therapeutic. The protein can also be used to raise antibodies useful
 CC in diagnosis and therapy
 XX
 XX Sequence 255 AA;
 SQ
 Query Match 87.1%; Score 1129; DB 5; Length 255;
 Best Local Similarity 92.5%; Pred. No. 4.2e-111;
 Matches 209; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 QY 14 GQASIPEDGGLFFLLCCIDRDWAVTCFAEEAFQALTDPSDLPSLFCNVHOSVFEEER 73
 DB 26 GQGHVPEDGGLFFLLCCIDRDWAVTCFAEEAFQAITDNDLPSLFCNVHOSVFEGEE 85
 QY 74 SKEKFEGLPRTYDECVTQFQFKSFRVRINFSPKSAARARIELHETQFRGKLLPYFAQ 133
 DB 86 SKEKFEGLPRTYDCCVTQFQFKSFRVRINFSPKSAARARIELHETQFRGKLLPYFAQ 145
 QY 134 VQPTETDGDKLHLPQPAKQFLLISPPSSPVGWKQIPISATPVINVDLYAVAKLGPGEK 193
 DB 146 VQPTETDGDKLHLPQPAKQFLLISPPSSPVGWQIPINDATPVINVDLYAVAKLGPGEK 205

QY 194 YELHAGTESPTSVVHVHVCSDMEREDPKTSPKPKINQTRRPLGP 239
 DB 206 YELHAGTESPTSVVHVHVCSDIEEDPKTSPKPKIQTTRRPLGP 251
 RESULT 4
 ADE37339
 ID ADE37339 standard; protein; 255 AA.
 XX
 XX ADE37339;
 XX
 XX 29-JAN-2004 (first entry)
 XX Human Down syndrome critical region 1-like lalpha protein.
 XX
 XX Down syndrome critical region 1-like lalpha protein; nontropic;
 KW neuroprotective; peptide therapy; gene therapy; Alzheimer's disease;
 KW human.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 11 /label= OTHER
 FT /note= "OTHER= Unknown or other amino acid; encoded by
 FT TNG"
 XX
 XX US2003186333-A1.
 XX
 XX 02-OCT-2003.
 XX
 XX 06-NOV-2002; 2002US-00290438.
 XX
 XX 11-JUL-2000; 2000US-00614474.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Loring JF, Tingley DW, Edwards CM, Streeter DG;
 XX WPI; 2003-811734/76.
 DR N-PSDB; ADE37338.
 XX
 XX New purified Down syndrome critical region 1-like 1 protein, used for
 PT diagnosing and treating Alzheimers disease, and for identifying and
 PT purifying antibodies that specific bind to the protein.
 XX
 XX Example 8; Fig 1; 39pp; English.
 PS
 XX This invention relates to a novel purified Down syndrome critical region
 CC 1-like 1 protein comprising a polypeptide having fully defined sequence
 CC of 255 amino acids, as given in the specification. Compounds which
 CC modulate the protein of the invention may have nontropic or
 CC neuroprotective activity. The protein sequence of the invention and the
 CC cDNA sequence which encodes it may be useful for peptide therapy and gene
 CC therapy respectively. The invention may prove useful in development of
 CC therapeutics for the treatment of Alzheimer's disease. The present
 CC sequence is the amino acid sequence of the human Down syndrome critical
 CC region 1-like lalpha protein of the invention. Note: This sequence is
 CC given as Seq ID2 in the sequence listing but is referred to as Seq ID1
 CC throughout the specification.
 XX
 XX Sequence 255 AA;
 SQ
 Query Match 87.1%; Score 1129; DB 7; Length 255;
 Best Local Similarity 92.5%; Pred. No. 4.2e-111;
 Matches 209; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 QY 14 GQASIPEDGGLFFLLCCIDRDWAVTCFAEEAFQALTDPSDLPSLFCNVHOSVFEEER 73
 DB 26 GQGHVPEDGGLFFLLCCIDRDWAVTCFAEEAFQAITDNDLPSLFCNVHOSVFEGEE 85
 QY 74 SKEKFEGLPRTYDECVTQFQFKSFRVRINFSPKSAARARIELHETQFRGKLLPYFAQ 133

```

Db      86  SKEKPEGLRTYDDCVTFQLFKSFRRVRINFSNPKSAARARIELHETQGRKKLKLKLYPAQ 145
QY      134  VQTPETDGDKLHLAPQPAKQFLISPPSPSVGWKPISDATPVNLYDLYAVAKLGPGBK 193
Db      146  VQTPETDGDKLHLAPQPAKQFLISPPSPSVGWQPIN DATPVNLYDLYAVAKLGPGBK 205
QY      194  YELHAGTESTPSSVVHVCDSDMEREDPKTSKPKINQTRRGLPP 239
Db      206  YELHAGTESTPSSVVHVCDSDIEEDPKTSKPKIIQTRRGLPP 251

RESULT 5
AAE18913
ID  AAE18913 standard; protein; 197 AA.
XX
AC  AAE18913;
XX
DT  17-MAY-2002 (first entry)
XX
DE  Mouse MCIP associated proein #4.
XX
KW  Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;
KW  heart failure; cardiomyopathy; heart disease; mouse.
XX
OS  Mus musculus.
XX
PN  WO200204491-A2.
XX
PD  17-JAN-2002.
XX
PF  06-JUL-2001; 2001WO-US021662.
XX
PR  07-JUL-2000; 2000US-0216601P.
XX
PS  13-FEB-2001; 2001US-00782953.
XX
PA  (TEXA ) UNIV TEXAS SYSTEM.
PA  (WILL/) WILLIAMS S R.
PA  (ROTH/) ROTHERMEL B.
XX
PI  Williams SR, Rothermel B;
XX
WPI: 2002-179698/23.
DR  N-PSDB; AAD30154.
XX

Screening for modulators of muscle calcineurin interacting protein (MCIP)
binding, expression or phosphorylation, useful for treating cardiac
hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a
test compound.
PS  Disclosure; Page 154; 174pp; English.
XX

The invention relates to muscle calcineurin interacting proteins (MCIPs)
and nucleic acid molecules encoding such proteins. MCIPs form a physical
complex with the catalytic subunit of calcineurin and increased levels of
MCIPs correspond to a reduced ability of calcineurin to stimulate
transcription of certain target genes. The invention also relates to
methods for identifying modulators of MCIP binding, expression or
phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin
may be used for treating cardiac hypertrophy and heart failure.
CC  Antibodies to MCIP can be used in characterising the MCIP content of
CC  healthy and diseased tissues and subsequently for determining the
CC  presence or absence of cardiomyopathy or as predictor of heart disease.
CC  The present sequence is mouse MCIP associated protein. Note: This
CC  sequence has been described as mouse MCIP2 encoding DNA in the
CC  specification, however the sequence seems to be a MCIP associated protein
XX
SQ  Sequence 197 AA;

Query Match      68.1%; Score 882; DB 5; Length 197;
Best Local Similarity 91.8%; Pred. No. 5.2e-85;
Matches 168; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY      57  NSLFACNVHQSVFEEESKEKFEGLFRTYDECVTQFLFKSFRRVRINFSHPKSAARARIE 116

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Db      11  STLVAQVVDVVEFTNQEVKEKPEGLFRTYDECVTQFLFKSFRRVRINFSHPKSAARARIE 70
QY      117  LHETQFRGKKLPLYFAQVQTPTDGDKLHLAPPQPAKQFLISPPSPSVGWKPISDATPV 176
Db      71  LHETQFRGKKLPLYFAQVQTPTDGDKLHLAPPQPAKQFLISPPSPSVGWKPISDATPV 130
QY      177  LNYDLLYAVAKLGPGEKYLHAGTESTPSSVVHVCDSDMEREDPKTSKPKINQTRRPP 236
Db      131  LNYDLLYAVAKLGPGEKYLHAGTESTPSSVVHVCDSDMEREDPKTSKPKIIQTRRPP 190
QY      237  LPP 239
Db      191  LPP 193

RESULT 6
ABO07172
ID  ABO07172 standard; protein; 197 AA.
XX
AC  ABO07172;
XX
DT  13-AUG-2003 (first entry)
XX
DE  Human p53 modifying protein, SEQ ID 132.
XX
KW  Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
KW  antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;
KW  lung cancer; ovarian cancer; angiogenesis; cell cycle;
KW  apoptotic disorder; cell proliferation disorder.
XX
OS  Homo sapiens.
XX
PN  WO200299122-A1.
XX
PD  12-DEC-2002.
XX
PF  03-JUN-2002; 2002WO-US017382.
XX
PR  05-JUN-2001; 2001US-0296076P.
PR  10-OCT-2001; 2001US-0328605P.
PR  15-FEB-2002; 2002US-0357253P.
XX
PA  (EXEL-) EXELIXIS INC.
XX
PI  Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
XX
WPI: 2003-156859/15.
DR  N-PSDB; ACD13348.
XX

Identifying modulators of the p53 pathway for use in treating apoptotic
or cell proliferation disorders, comprises screening for agents that
modulate activity of a human ortholog of genes that modify the p53
pathway in Drosophila.
XX
Example 2; Page 434-435; 678pp; English.
XX

The invention relates to identifying (M1) a candidate p53 pathway
modulating agent, by contacting an assay system comprising a purified HM
polypeptide (human orthologue of genes that modify the p53 pathway in
Drosophila) or nucleic acid with a test agent under conditions, where but
for the presence of the test agent, the system provides a reference
activity, and detecting a test agent-biased activity of a cell (comprising
Also included are modulating (M2) a p53 pathway of a cell (comprising
contacting a cell defective in p53 function with a candidate modulator
that specifically binds to a HM polypeptide comprising an HM amino acid
sequence, where p53 function is restored), modulating (M3) a p53 pathway
in a mammalian cell (comprising contacting the cell with an agent that
specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
a disease in a patient (comprising: (a) obtaining a biological sample
from the patient; (b) contacting the sample with a probe for HM
expression; (c) comparing the results with a control; and (d) determining
whether the comparison indicates a likelihood disease). (M1) is useful

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CC for identifying modulators of the p53 pathway. A probe for HM expression
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
 CC in a patient where the cancer has greater than 25 % expression level.
 CC Modulators identified by (M1) are useful in a variety of diagnostic and
 CC therapeutic applications, where disease or disorder prognosis is related
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
 CC the p53 function of the cell, so that the cell undergoes normal
 CC proliferation or progression through the cell cycle. (M2) and (M3) are
 CC also useful for treating defects in the p53 pathway such as angiogenic,
 CC apoptotic or cell proliferation disorders. The present sequence
 CC represents a human p53 pathway modifying protein
 XX
 XX Sequence 197 AA;

Query Match 66.4%; Score 861; DB 6; Length 197;
 Best Local Similarity 89.1%; Pred. No. 8.9e-83;
 Matches 163; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 57 NSLFACNVHQSVEEESKEKEGFLRTYDECVTQFLEKSFRRVRINFNPKSAARARIE 116
 DB 11 STLVACVDVVEFTNQEVKEKEGFLRTYDCCVTQFLEKSFRRVRINFNPKSAARARIE 70
 QY 117 LHETQFRGKKLPLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPSVGMKPISDATPV 176
 DB 71 LHETQFRGKKLPLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPSVGMKPISDATPV 130
 QY 177 LNYDLLYAVAKLPGKEKYLHAGTSTPSVHVHVCSDMEREDPKTSKPKNQTRRPG 236
 DB 131 LNYDLLYAVAKLPGKEKYLHAGTSTPSVHVHVCSDMEREDPKTSKPKNQTRRPG 190
 QY 237 LPP 239
 DB 191 LPP 193

RESULT 7
 AAE18916
 ID AAE18916 standard; protein; 192 AA.
 XX
 AC AAE18916;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Human MCIP associated protein #3.
 XX
 KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;
 KW heart failure; cardiomyopathy; heart disease; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200204491-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 06-JUL-2001; 2001WO-US021662.
 XX
 PR 07-JUL-2000; 2000US-0216601P.
 PR 13-FEB-2001; 2001US-00782953.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (WILL/) WILLIAMS S R.
 PA (ROTH/) ROTHERMEL B.
 XX
 PI Williams SR, Rothermel B;
 XX
 DR WPI; 2002-179698/23.
 DR N-PSDB; AAD30157.
 XX

Screening for modulators of muscle calcineurin interacting protein (MCIP)
 PT binding, expression or phosphorylation, useful for treating cardiac
 PT hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a

PT test compound.
 XX
 PS Example 1; Page 165-166; 174pp; English.
 XX
 CC The invention relates to muscle calcineurin interacting proteins (MCIPs)
 CC and nucleic acid molecules encoding such proteins. MCIPs form a physical
 CC complex with the catalytic subunit of calcineurin and increased levels of
 CC MCIPs correspond to a reduced ability of calcineurin to stimulate
 CC transcription of certain target genes. The invention also relates to
 CC methods for identifying modulators of MCIP binding, expression or
 CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin
 CC may be used for treating cardiac hypertrophy and heart failure.
 CC Antibodies to MCIP can be used in characterising the MCIP content of
 CC healthy and diseased tissues and subsequently for determining the
 CC presence or absence of cardiomyopathy or as predictor of heart disease.
 CC The present sequence is human MCIP associated protein. Note: This
 CC sequence has been described as human MCIP splice variant in
 CC specification, however the sequence seems to be a MCIP associated protein
 XX
 XX Sequence 192 AA;

Query Match 65.4%; Score 848; DB 5; Length 192;
 Best Local Similarity 88.0%; Pred. No. 2.1e-81;
 Matches 161; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 57 NSLFACNVHQSVEEESKEKEGFLRTYDECVTQFLEKSFRRVRINFNPKSAARARIE 116
 DB 6 STLVACVDVVEFTNQEVKEKEGFLRTYDCCVTQFLEKSFRRVRINFNPKSAARARIE 65
 QY 117 LHETQFRGKKLPLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPSVGMKPISDATPV 176
 DB 66 LHETQFRGKKLPLYFAQVQTPETDGDGKLHLAPPQPAKQFLISPPSSPSVGMKPISDATPV 125
 QY 177 LNYDLLYAVAKLPGKEKYLHAGTSTPSVHVHVCSDMEREDPKTSKPKNQTRRPG 236
 DB 126 LNYDLLYAVAKLPGKEKYLHAGTSTPSVHVHVCSDMEREDPKTSKPKNQTRRPG 185
 QY 237 LPP 239
 DB 186 LPP 188

RESULT 8
 ADE37341
 ID ADE37341 standard; protein; 192 AA.
 XX
 AC ADE37341;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Down syndrome critical region 1-like 1 protein.
 XX
 KW Down syndrome critical region 1-like alpha protein; neurotropic;
 KW neuroprotective; peptide therapy; gene therapy; Alzheimer's disease;
 KW human; Down syndrome critical region 1-like 1 protein.
 XX
 OS Homo sapiens.
 XX
 PN US2003186333-A1.
 XX
 PD 02-OCT-2003.
 XX
 PF 06-NOV-2002; 2002US-00290438.
 XX
 PR 11-JUL-2000; 2000US-00614474.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Loring JF, Tingley DW, Edwards CM, Streeter DG;
 XX
 DR WPI; 2003-811734/76.
 XX
 PT New purified Down syndrome critical region 1-like 1 protein, used for

QY 55 LPNSLFACNVHQSVEEESKEKFEGLFRITYDECVTFQLFKSPRRVRINFSPKSAAR 114
 Db 64 LPSATTACHLDPRVFDGLCKRAKESLFRITYDKDITFQYKFSKRVIRINFSPFSAADAR 123
 QY 115 IEHETQFRGKKLPLYFAQVQTPETDGDKLHLAPPQAKQFLISPPSSVGVKPI 174
 Db 124 LQHLKTEFLGKEMKLYFAQTLHGSS----HLAPPNPDQKFLISPPASPPVGVKQVEDAT 179
 QY 175 PVLYNYDLLYAVAKLGPGEKYLHAGTSTPSVVHVCDSDMEREDPKTS---PKPKIN 230
 Db 180 PVLYNYDLLYAVAKLGPGEKYLHAGTSTPSVVHVCDSDMEREDPKTS---PKPKIN 230
 QY 231 QTRRPLPP 239
 Db 240 QTRRPEYTP 248

RESULT 14
 AAE18915
 ID AAE18915 standard; protein; 197 AA.
 AC AAE18915;
 XX
 DT 17-MAY-2002 (first entry)
 DE
 XX Human MCIP associated protein #2.
 XX
 KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;
 KW heart failure; cardiomyopathy; heart disease; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200204491-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 06-JUL-2001; 2001WO-US021662.
 XX
 PR 07-JUL-2000; 2000US-0216601P.
 PR 13-FEB-2001; 2001US-00782953.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (WILL/) WILLIAMS S R.
 PA (ROTH/) ROTHERMEL B.
 XX
 PI Williams SR, Rothermel B;
 XX
 DR WPI; 2002-179698/23.
 DR N-PSDB; AAD30156.
 XX
 PT Screening for modulators of muscle calcineurin interacting protein (MCIP)
 PT binding expression or phosphorylation, useful for treating cardiac
 PT hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a
 PT test compound.
 XX
 PS Example 1; Page 161-162; 174pp; English.
 XX
 CC The invention relates to muscle calcineurin interacting proteins (MCIPs)
 CC and nucleic acid molecules encoding such proteins. MCIPs form a physical
 CC complex with the catalytic subunit of calcineurin and increased levels of
 CC MCIPs correspond to a reduced ability of calcineurin to stimulate
 CC transcription of certain target genes. The invention also relates to
 CC methods for identifying modulators of MCIP binding, expression or
 CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin
 CC may be used for treating cardiac hypertrophy and heart failure.
 CC Antibodies to MCIP can be used in characterizing the MCIP content of
 CC healthy and diseased tissues and subsequently for determining the
 CC presence or absence of cardiomyopathy or as predictor of heart disease.
 CC The present sequence is human MCIP associated protein. Note: This
 CC sequence has been described as murine MCIP splice variant in the
 CC specification, however the sequence seems to be a MCIP associated protein
 XX Sequence 197 AA;
 SQ

Query Match 47.5%; Score 616; DB 5; Length 197;
 Best Local Similarity 61.1%; Pred. No. 9.8e-5;
 Matches 118; Conservative 28; Mismatches 39; Indels 8; Gaps 2;
 QY 51 DFSDLPSLAFACNVHQSVEEESKEKFEGLFRITYDECVTFQLFKSPRRVRINFSPKSA 110
 Db 5 DLQDLPSATTACHLDPRVFDGLCKRAKESLFRITYDKDITFQYKFSKRVIRINFSPFSA 64
 QY 111 APARIELHETQFRGKKLPLYFAQVQTPETDGDKLHLAPPQAKQFLISPPSSVGVKPI 170
 Db 65 ADARLQHLKTEFLGKEMKLYFAQTLHGSS----HLAPPNPDQKFLISPPASPPVGVKQV 120
 QY 171 SDATPVLYNYDLLYAVAKLGPGEKYLHAGTSTPSVVHVCDSDMEREDPKTS---PK 226
 Db 121 EDATPVLYNYDLLYAVAKLGPGEKYLHAGTSTPSVVHVCDSDMEREDPKTS---PK 226
 QY 227 PKINQTRRPLPP 239
 Db 181 PKIQTTRRPEYTP 193

RESULT 15
 AAE18914
 ID AAE18914 standard; protein; 197 AA.
 AC AAE18914;
 XX
 DT 17-MAY-2002 (first entry)
 DE
 XX Human MCIP associated protein #1.
 XX
 KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;
 KW heart failure; cardiomyopathy; heart disease; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200204491-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 06-JUL-2001; 2001WO-US021662.
 XX
 PR 07-JUL-2000; 2000US-0216601P.
 PR 13-FEB-2001; 2001US-00782953.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (WILL/) WILLIAMS S R.
 PA (ROTH/) ROTHERMEL B.
 XX
 PI Williams SR, Rothermel B;
 XX
 DR WPI; 2002-179698/23.
 DR N-PSDB; AAD30155.
 XX
 PT Screening for modulators of muscle calcineurin interacting protein (MCIP)
 PT binding expression or phosphorylation, useful for treating cardiac
 PT hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a
 PT test compound.
 XX
 PS Example 1; Page 157-158; 174pp; English.
 XX
 CC The invention relates to muscle calcineurin interacting proteins (MCIPs)
 CC and nucleic acid molecules encoding such proteins. MCIPs form a physical
 CC complex with the catalytic subunit of calcineurin and increased levels of
 CC MCIPs correspond to a reduced ability of calcineurin to stimulate
 CC transcription of certain target genes. The invention also relates to
 CC methods for identifying modulators of MCIP binding, expression or
 CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin
 CC may be used for treating cardiac hypertrophy and heart failure.
 CC Antibodies to MCIP can be used in characterizing the MCIP content of
 CC healthy and diseased tissues and subsequently for determining the
 CC presence or absence of cardiomyopathy or as predictor of heart disease.
 CC

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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:22:55 ; Search time 33 Seconds
(without alignments)
547.426 Million cell updates/sec

Title: US-09-575-580B-5
Perfect score: 1296
Sequence: 1 EFVDPRVRRLGQASIP.....TSPKINQTRRGLPPFGH 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1129	87.1	255	4	US-09-614-474-2
2	861	66.4	206	4	US-09-949-016-11450
3	848	65.4	192	4	US-09-614-474-10
4	848	65.4	192	4	US-09-949-016-6659
5	708.5	54.7	241	4	US-09-614-474-11
6	708.5	54.7	248	4	US-09-949-016-7081
7	575	44.4	171	4	US-09-949-016-6493
8	575	44.4	173	4	US-09-949-016-11053
9	565	43.6	171	2	US-08-665-040-2
10	405.5	31.3	289	4	US-09-270-767-44503
11	312	24.1	111	4	US-09-513-999C-5849
12	106.5	8.2	285	4	US-09-248-796A-19049
13	106.5	8.2	767	4	US-09-248-796A-15612
14	94	7.3	655	3	US-09-347-833-4
15	89	6.9	905	2	US-08-574-959A-9
16	89	6.9	905	3	US-09-357-014-9
17	89	6.9	1135	2	US-08-574-959A-7
18	89	6.9	1135	3	US-09-357-014-7
19	88.5	6.8	782	4	US-09-252-991A-30464
20	88.5	6.8	4019	4	US-09-854-133-425
21	85	6.6	454	3	US-08-348-518C-4
22	85	6.6	454	3	US-08-476-509B-4
23	84.5	6.5	1106	1	US-08-180-195-2
24	84.5	6.5	1106	1	US-08-188-317-2
25	84.5	6.5	1106	1	US-08-477-329-2
26	84.5	6.5	1106	2	US-08-475-458-2
27	84.5	6.5	1106	2	US-08-460-510-2

28	84.5	6.5	1106	2	US-08-460-490-2	Sequence 2, Appli
29	84.5	6.5	1106	3	US-08-980-400-2	Sequence 2, Appli
30	84.5	6.5	1106	3	US-08-462-728-4	Sequence 2, Appli
31	84.5	6.5	1106	3	US-09-583-459A-2	Sequence 2, Appli
32	84.5	6.5	1106	3	US-09-583-210-2	Sequence 2, Appli
33	84.5	6.5	1106	3	US-09-583-449A-2	Sequence 2, Appli
34	84.5	6.5	1106	3	US-09-435-059-2	Sequence 2, Appli
35	84.5	6.5	1106	3	US-08-461-917-4	Sequence 4, Appli
36	84.5	6.5	1106	4	US-08-464-436-4	Sequence 4, Appli
37	84.5	6.5	1106	4	US-08-464-436-4	Sequence 4, Appli
38	84.5	6.5	1106	4	US-09-866-510-16	Sequence 16, Appli
39	84.5	6.5	1106	4	US-09-866-510-18	Sequence 18, Appli
40	84.5	6.5	1106	4	US-09-866-510-20	Sequence 20, Appli
41	84.5	6.5	1106	4	US-09-866-510-22	Sequence 22, Appli
42	84.5	6.5	1106	5	PCT-US92-00730-2	Sequence 2, Appli
43	84.5	6.5	1106	5	PCT-US92-00862-2	Sequence 2, Appli
44	84	6.5	428	3	US-09-347-833-6	Sequence 6, Appli
45	83	6.4	566	1	US-08-810-116-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-09-614-474-2
; Sequence 2, Application US/09614474
; Patent No. 6524819
; GENERAL INFORMATION:

; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debra W.
; APPLICANT: Edwards, Carla M.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION. 1-LIKE PROTEINS
; FILE REFERENCE: PC-0013 US
; CURRENT APPLICATION NUMBER: US/09/614,474
; CURRENT FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRI
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Inocyte ID No. 6524819 247500.5
; NAME/KEY: unsure
; LOCATION: 11
; OTHER INFORMATION: unknown or other
US-09-614-474-2

Query Match	87.1%	Score 1129;	DB 4;	Length 255;
Best Local Similarity	92.5%	Pred. No. 1.5e-121;		
Matches	209;	Conservative	9;	Mismatches 8;
				Indels 0;
				Gaps 0;
QY	14	GQASIPEDGGLPFLCCIDRDMAVTCFAEEAFQALTFSDLSLFCNVHQSVEEEE	73	
Db	26	GQGHVPEDGGLPFLCCIDRDMAVTCFAEEAFQALTFSDLSLFCNVHQSVEEEE	85	
QY	74	SKEKFGRLFRTYDECVTFQFLKFSFRVRINFSPKSAARARIELHETQFRGKKLPLFAQ	133	
Db	86	SKEKFGRLFRTYDDCVTFQFLKFSFRVRINFSPKSAARARIELHETQFRGKKLPLFAQ	145	
QY	134	VQPTDGDGKLHAPQPAKQFLISPPSSPVGKPTSDATPVNLYLVAVAKLGPGEK	193	
Db	146	VQPTDGDGKLHAPQPAKQFLISPPSSPVGKPTSDATPVNLYLVAVAKLGPGEK	205	
QY	194	YELHAGTSTPSVVHVHVCSDMEREDPKTSPKPKINQTRRGLPP	239	
Db	206	YELHAGTSTPSVVHVHVCSDMEREDPKTSPKPKINQTRRGLPP	251	

RESULT 2
US-09-949-016-11450

	Query Match	44.4%;	Score 575;	DB 4;	Length 173;
	Best Local Similarity	65.9%;	Pred. No. 5.6e-58;		
	Matches 110;	Conservative 22;	Mismatches 27;	Indels 8;	Gaps 2
Qy	77	KEEGLPRTYDECVTQLFKSPRRVRVINESHPKSAARARIELHETQFRGKKLPLYFPAQVOT	136		
Db	7	KESLPRTYDKDITQYFKSPKRVVINESPNFSAADARLOLHKTEFGKEMKLYPAQTJLH	66		
Qy	137	PETDGDGLHAPPQPAKQFLISPPSSPVGWKPISDATPVNYDLYAVAKLPBGKEYEL	196		
Db	67	IGSS---HLAPNPDKQLISPPASPVGWKQVEDATPVNYDLYATSKLGFGEKEYEL	122		
Qy	197	HAGTSTPSVVVHVCDSDMEREEDPKTS-----PKPKINQTRRRPGLPP	239		
Db	123	HAATDTTPSVVVHVCSDOEKKEEEMERMRRPKKIIOTRRPEYTP	169		

```

RESULT 9
US-08-665-040-2
; Sequence 2, Application US/08665040
; Patent No. 5869318
; GENERAL INFORMATION:
; APPLICANT: ESTIVILL PALLEJA, XAVIER
; APPLICANT: FUENTES, JUAN JOSE
; APPLICANT: PRITCHARD, MELANIE
; TITLE OF INVENTION: A NEW GENE SEQUENCE OF THE
; TITLE OF INVENTION: DOWN SYNDROM CRITICAL REGION OF HUMAN CHROMOSOME 21,
; TITLE OF INVENTION: IDENTIFIED BY A NEW "ALU-SPICING PCR" TECHNIQUE,
; TITLE OF INVENTION: CODING FOR A PROLINE-RICH PROTEIN (DSCR1) HIGHLY
; TITLE OF INVENTION: EXPRESSED IN FOSTER BRAIN AND IN HEART AND METHOD
; TITLE OF INVENTION: FOR CHARACTERIZING IT.

```

Query Match 43.6%; Score 565; DB 2; Length 171;
Best Local Similarity 65.3%; Pred. No. 7.8e-57;
Matches 109; Conservative 22; Mismatches 28; Indels 8; Gaps 2

[illegible]

```

RESULT 10
US-09-270-767-44503
; Sequence 44503, Application US/09270767
; Patent NO. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44503
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44503

```

Query Match	31.3%	Score 405.5;	DB 4;	Length 289;
Best Local Similarity	41.2%;	Pred. No. 4.1e-38;		
Matches 89;	Conservative 32;	Mismatches 74;	Indels 21;	Gaps 6
Qy	15	QQASIPBDGGLFFLCCIDRWAVTQCFAEAFQALTD	FDLSPLSLFACNVHQSFVEEES	74
Db	94	QHPSLPKEGD-----VDSD-----TEPEVDA	DSFDDDLPTGIIVTNIHSEVPANDEL	139
Qy	75	KEKPEGUFRYDECVTFQLPKFSFRVRINFSHPK	SAARARIELHETQPRGKK-IPLYPAQ	133
Db	140	KHAMEELFTFSSATPQWLRSFRLRVYNDNAIAA	NARIKLGHEYEFNKATVTICYPAQ	199
Qy	134	VQPTETDGDKLHLIAPPOPAKQFLLSPSSSVG	WKPISDATPVNLNLLYAVAKLGPCK	193
Db	200	PVTPVSN---XNQLQPPAPVQFLISPPASPPAG	WEPREEGEPLVNHDLIAALSLTTPGS	256
Qy	194	YELHAGTESTPSVVVHVCDSDMEREEDPKTSPK	PKI	229
Db	257	HELHPOSEDPAIIVHTA---MLAETGFGLOVKAP	I	289

```

RESULT 11
US-09-513-999C-5849
; Sequence 5849, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5849
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5849

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; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15612
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (764)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations
US-09-248-796A-15612

Query Match      8.2%; Score 106.5; DB 4; Length 767;
Best Local Similarity 23.2%; Pred. No. 0.005;
Matches 45; Conservative 35; Mismatches 75; Indels 39; Gaps 8

Qy      63 NVHQSVPEESKEK--FEGIFR-TYD-----ECVTQLFKS-FRRVRINFSH 106
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      240 DVNETVFQDKPKQSNIFKLLRKNHDDVHPHIERIQKEQIDWATFKSDINRMNLSLTS 299
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      107 PKSAARARIELHETQFRGKGLPLYFAQVQTPETDG--DKLHLAPPQAPAKQLISPPSSP 163
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      300 DKOSRTKRVVRQDGSIIIVKPLD-FISEINTNETVGPEDDDIDLENVQYSK----- 348
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      164 SVGWKPTSDATPVNLVYDLLYAVAKLGPGEKYELHAGT-ESTPSVVVHVCDSDMEREEDPK 222
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      349 -----IETFMLNYDLSYDLNELISDISIKFHSSVINQVRCILVHLCKFDIIEETSKI 400
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      223 TSPKPKINQTRRPQ 236
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      401 LOOKPKLSEVQHSQ 414

RESULT 14
US-09-347-833-4
; Sequence 4, Application US/09347833
; Patent No. 6294658
; GENERAL INFORMATION:
; APPLICANT: Farnodu, Layo O.
; APPLICANT: Odell, Joan T.
; TITLE OF INVENTION: Factors Involved in Gene Expression
; FILE REFERENCE: BB-1172
; CURRENT APPLICATION NUMBER: US/09/347,833
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,415
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-347-833-4

Query Match      7.3%; Score 94; DB 3; Length 655;
Best Local Similarity 21.4%; Pred. No. 0.11;
Matches 55; Conservative 33; Mismatches 91; Indels 78; Gaps 13

Qy      32 DRDVAVTQCFAE-----EAFQA-LTDFSD--LPNSLFACNVHQSVFEESKEKF 78
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      280 DKEWYV--CRAQKKSEREMELKEKFEKNIKEAADKNQGTNLYLKNLDDSIDDEKLKEIF 337
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      79 EGLFRFYDECVTQLFKSFRVR-----INFSPKSAARARIELHETQFRGKGLPLYFAQ 133
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      338 AD-FGTITSC---KVMRDNLNGSVKGSFGVAFKSAEDASRALVAMNGMIGSK--PLYVAL 391
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      134 VQFPETDGDKLH-----LAPPAQAKQLISPPSSPSVGWKPISDATPVNLVYLLYA 184
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      392 AQKERRARKLAQFQSMRRPMVMPSPSVAPRNPMTIPGVGVGQQLFYGQPPP----- 444
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      185 VAKLGPGEKYELHAGTSTPSVVVHVCDSDMEREEDPKTSP-----KPKINQTRRPGLP- 238
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 445 FVNQFGFGFQQLIPGMRPSV-----GPIPNFVMVMVQGGQPPQRPDA 487
QY 239 -----PFGH 242
Db 488 GRRAGTGGIQQPMPMGH 504

RESULT 15
US-08-574-959A-9
; Sequence 9, Application US/08574959A
; Patent No. 5962224
; GENERAL INFORMATION:
; APPLICANT: Jackyoon Shin, Insil Joong, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 905 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-574-959A-9

Query Match 6.9%; Score 89; DB 2; Length 905;
Best Local Similarity 24.0%; Pred. No. 0.66;
Matches 41; Conservative 16; Mismatches 82; Indels 32; Gaps 5;
QY 70 EEESKEKPEGLFRITYDECVTQLFKSFRVRVINFSPKSAARARIELHETQFRGKLP 129
Db 698 EEEEEEEFEFEFEFG-----ELEEEEEEEEEELEVE----- 736
QY 130 YFAQVQTPTDGDKHLHAPPQAKFLISPPSSPSVGWKPISDATPVLYDLYAVAKLG 189
Db 737 ---DLEFGTAGGEVEGAPPTLPALPPESP-----PKVQPEPEPEPGILLVEE-- 786
QY 190 PGKEYELHAGTSTPSVVHVHCDSDMERE-EDPKTSPKPKINQTRRRPGLPP 239
Db 787 PGTEERGADTAPTALPEALPSQGEVEREGESPAAGPPPPQELVEEPEKXP 837

Search completed: November 16, 2005, 16:31:57
Job time : 34 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2005, 16:22:57 ; Search time 123.2 Seconds
(without alignments)
821.876 Million cell updates/sec

Title: US-09-575-580B-5

Perfect score: 1296

Sequence: 1 EFVDRVRPRVRLGQASIP.....TSPKPKINOTRRPGLPRGH 242

Scoring table: BLOSUM62

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Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10F_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1129	87.1	243	15	US-10-104-047-2216
2	1129	87.1	255	14	US-10-290-438-2
3	882	68.1	197	9	US-09-782-953-9
4	882	68.1	197	9	US-09-782-953-10
5	848	65.4	192	9	US-09-782-953-18
6	848	65.4	192	9	US-09-782-953-19
7	848	65.4	192	14	US-10-290-438-10
8	848	65.4	197	18	US-10-764-425-126
9	708.5	54.7	241	9	US-09-782-953-21
10	708.5	54.7	241	9	US-09-782-953-22
11	708.5	54.7	241	14	US-10-290-438-11

12	676.5	52.2	212	9	US-09-782-953-24	Sequence 24, Appl
13	676.5	52.2	212	9	US-09-782-953-25	Sequence 25, Appl
14	648	50.0	252	15	US-10-104-047-2892	Sequence 2892, Ap
15	616	47.5	197	9	US-09-782-953-12	Sequence 12, Appl
16	616	47.5	197	9	US-09-782-953-13	Sequence 13, Appl
17	616	47.5	197	9	US-09-782-953-15	Sequence 15, Appl
18	616	47.5	197	9	US-09-782-953-16	Sequence 16, Appl
19	616	47.5	197	14	US-10-247-671-174	Sequence 174, Appl
20	616	47.5	197	16	US-10-755-889-120	Sequence 120, Appl
21	613.5	47.3	198	9	US-09-782-953-6	Sequence 6, Appl
22	613.5	47.3	198	9	US-09-782-953-7	Sequence 7, Appl
23	606.5	46.8	198	9	US-09-782-953-3	Sequence 3, Appl
24	606.5	46.8	198	9	US-09-782-953-4	Sequence 4, Appl
25	575	44.4	171	15	US-10-428-487-24	Sequence 24, Appl
26	418.5	32.3	292	20	US-11-097-143-41193	Sequence 41193, A
27	289	22.3	142	9	US-09-925-302-790	Sequence 790, App
28	289	22.3	142	10	US-09-925-302-790	Sequence 790, App
29	213	16.4	58	9	US-09-864-761-35379	Sequence 35379, A
30	213	16.4	58	9	US-09-864-761-43076	Sequence 43076, A
31	168	13.0	56	9	US-09-864-761-34111	Sequence 34111, A
32	101	7.8	32	14	US-10-194-155-8	Sequence 8, Appli
33	98.5	7.6	608	17	US-10-732-923-13425	Sequence 13425, A
34	98.5	7.6	922	15	US-10-042-865-96	Sequence 96, Appl
35	98.5	7.6	922	15	US-10-263-929-190	Sequence 190, App
36	98.5	7.6	948	13	US-10-087-192-1869	Sequence 1869, Ap
37	98.5	7.6	1066	15	US-10-042-865-95	Sequence 95, Appl
38	98.5	7.6	1066	17	US-10-732-923-13684	Sequence 13684, A
39	98.5	7.6	1077	17	US-10-732-923-13426	Sequence 13426, A
40	98.5	7.6	1096	15	US-10-210-130-130	Sequence 130, App
41	98.5	7.6	1097	15	US-10-288-798-12	Sequence 12, Appl
42	98.5	7.6	1097	15	US-10-362-892-12	Sequence 12, Appl
43	98.5	7.6	1118	15	US-10-112-944-259	Sequence 259, Appl
44	97.5	7.5	1024	15	US-10-042-865-16	Sequence 16, Appl
45	96.5	7.4	248	15	US-10-425-114-48915	Sequence 48915, A

ALIGNMENTS

RESULT 1
US-10-104-047-2216
; Sequence 2216, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2216
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2216

Query Match	87.1%	Score 1129;	DB 15;	Length 243;
Best Local Similarity	92.5%	Pred. No. 2.2e-105;		
Matches 209;	Conservative	9;	Mismatches 8;	Indels 0; Gaps 0;
QY	14	QQQASIPEDGGLFFICCIDRDWAVTQCFAEBAFQALTDPSDLPSLFCACNVHQSVFEEB	73	
Db	14	QQQGHVPEDGGLFFICCIDRDWAVTQCFAEBAFQAITDFNDLPNSLFCACNVHQSVFEEB	73	
QY	74	SKEPEGLFRYDECVTFQLEKSRVRVINFESHPSAARARIELHETQFRGKLLPYFAQ	133	
Db	74	SKEPEGLFRYDDCVTFQLEKSRVRVINFSPKSAARARIELHETQFRGKLLPYFAQ	133	
QY	134	VQTPETDGDGLHAPPQPAKQFLISPPSSPSVGMKPISDATPVLLNYDLLYAVAKLPGGEK	193	

Db 134 VOTPETDGDKLHLAPPQAKQFLISPPSPVGVQWQPIN DATPVLNVDLLYAVAKLGPGEK 193
QY 194 YELHAGTESTPSVVHVCDSDMEREDPKTSKPKNQTRRGLPP 239
Db 194 YELHAGTESTPSVVHVCDSDIEEBEDPKTSKPKNQTRRGLPP 239

RESULT 2

US-10-290-438-2
; Sequence 2, Application US/10290438
; Publication No. US20030186333A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEIN
; FILE REFERENCE: PC-0013-1C1P
; CURRENT APPLICATION NUMBER: US/10/290,438
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 09/614,474
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030186333A1 247500.5
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 11
; OTHER INFORMATION: unknown or other
US-10-290-438-2

Query Match 87.1%; Score 1129; DB 14; Length 255;
Best Local Similarity 92.5%; Pred. No. 2.3e-105;
Matches 209; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 14 GOQASIPEDGGLFELCCIDRDWAVTCFAEEAFQALTFPSDLNLSFACNVHQSVFEE 73
Db 26 GOQHVPEDGGLFELCCIDRDWAVTCFAEEAFQAITFDNLPNSLFACNVHQSVFEE 85
QY 74 SKEPEGLFRTYDECVTFQLFKSPRRVRINFSPKSAARARIELHETQFRGKLLPYFAQ 133
Db 86 SKEPEGLFRTYDDCVTFQLFKSPRRVRINFSPKSAARARIELHETQFRGKLLPYFAQ 145
QY 134 VOTPETDGDKLHLAPPQAKQFLISPPSPVGVQWQPIN DATPVLNVDLLYAVAKLGPGEK 193
Db 146 VOTPETDGDKLHLAPPQAKQFLISPPSPVGVQWQPIN DATPVLNVDLLYAVAKLGPGEK 205
QY 194 YELHAGTESTPSVVHVCDSDMEREDPKTSKPKNQTRRGLPP 239
Db 206 YELHAGTESTPSVVHVCDSDIEEBEDPKTSKPKNQTRRGLPP 251

RESULT 3

US-09-782-953-9
; Sequence 9, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSD:674P21
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-782-953-9

Query Match 68.1%; Score 882; DB 9; Length 197;
Best Local Similarity 91.8%; Pred. No. 1.5e-80;
Matches 168; Conservative 3; Mismatches 12; Indels 0; Gaps 0;
QY 57 NSLFACNVHQSVFEEESKEKEFGLFRITYDECVTFQLFKSPRRVRINFSPKSAARARIE 116
Db 11 STLAVACVVDVEFTNQEVKEKEFGLFRITYDECVTFQLFKSPRRVRINFSPKSAARARIE 70
QY 117 LHETQFRGKLLPYFAQVOTPETDGDKLHLAPPQAKQFLISPPSPVGVQWQPIN DATPV 176
Db 71 LHETQFRGKLLPYFAQVOTPETDGDKLHLAPPQAKQFLISPPSPVGVQWQPIN DATPV 130
QY 177 LNYDLLYAVAKLGPGEKVELHAGTESTPSVVHVCDSDMEREDPKTSKPKNQTRRPG 236
Db 131 LNYDLLYAVAKLGPGEKVELHAGTESTPSVVHVCDSDMEREDPKTSKPKNQTRRPG 190
QY 237 LPP 239
Db 191 LPP 193

RESULT 4

US-09-782-953-10
; Sequence 10, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSD:674P21
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-782-953-10

Query Match 68.1%; Score 882; DB 9; Length 197;
Best Local Similarity 91.8%; Pred. No. 1.5e-80;
Matches 168; Conservative 3; Mismatches 12; Indels 0; Gaps 0;
QY 57 NSLFACNVHQSVFEEESKEKEFGLFRITYDECVTFQLFKSPRRVRINFSPKSAARARIE 116
Db 11 STLAVACVVDVEFTNQEVKEKEFGLFRITYDECVTFQLFKSPRRVRINFSPKSAARARIE 70
QY 117 LHETQFRGKLLPYFAQVOTPETDGDKLHLAPPQAKQFLISPPSPVGVQWQPIN DATPV 176
Db 71 LHETQFRGKLLPYFAQVOTPETDGDKLHLAPPQAKQFLISPPSPVGVQWQPIN DATPV 130
QY 177 LNYDLLYAVAKLGPGEKVELHAGTESTPSVVHVCDSDMEREDPKTSKPKNQTRRPG 236
Db 131 LNYDLLYAVAKLGPGEKVELHAGTESTPSVVHVCDSDMEREDPKTSKPKNQTRRPG 190
QY 237 LPP 239
Db 191 LPP 193
RESULT 5
US-09-782-953-18

Db 16 LCSTQEEBEMIFGENEDDLDEMMDLSLPTSLFACSVHEAVFEAREQKERPEALFTY 75
Qy 86 DECVTFQPKSFRVRINFSHPKSAARARIELHETQFRGKPLYPFAQVOTPETDGDKLH 145
Db 76 DDQVTFQPKSFRVRINFSKPEAAARARIELHETDFNGQKLKLYFAQVQMSGEVDRKSY 135
Qy 146 LAPPPAKOFLISPPSPSGVWKPISDATPVNLNLYLAVAKLPGCEKYLHAGTSTPS 205
Db 136 LLPPQPVKQFLISPPASPPGVWQSEDAMPVINYDLLCAVSKLPGCEKYLHAGTSTPS 195
Qy 206 VVVHVCDSMEREEDPKTSPPKPKINOTRRPGLP 238
Db 196 VVVHVCESETEEBEETK-NPKQKIATRPPDP 227

RESULT 12
US-09-782-953-24
; Sequence 24, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: US/09782,953
; CURRENT APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2001-02-13
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-953-24

Query Match 52.2%; Score 676.5; DB 9; Length 212;
Best Local Similarity 67.9%; Pred. No. 9.5e-60;
Matches 133; Conservative 18; Mismatches 34; Indels 11; Gaps 2;
Qy 43 BEAFQALTDPSLPSLACNVHQSVEEESKEKEGFLRTYDECVTFQPKSFRVRV 102
Db 14 EDDLDEMMDLSLPTSLFACSVHEAVFEAREQKERPEALFTYDDQVTFQPKSFRVRV 73
Qy 103 NFSHPKSAARARIELHETQFRGKPLYPFAQVOTPETDGDKLHAPPQPAKQFLISPPSS 162
Db 74 NFSKPEAAARARIELHETDFNGQKLKLYFAQ-----SYLLPPQPVKQFLISPPAS 123
Qy 163 PSVGWKPISDATPVNLNLYLAVAKLPGCEKYLHAGTSTPSVVHVCDSDMEREEDPK 222
Db 124 PPGWQKQSEDAMPVINYDLLCAVSKLPGCEKYLHAGTSTPSVVHVCESETEEBEETK 183
Qy 223 TSPKPKINOTRRPGLP 238
Db 184 -NPKQKIATRPPDP 198

RESULT 13
US-09-782-953-25
; Sequence 25, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; FILE REFERENCE: US/09782,953
; CURRENT APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2001-02-13
; PRIOR FILING DATE: 2000-07-07

; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-953-25

Query Match 52.2%; Score 676.5; DB 9; Length 212;
Best Local Similarity 67.9%; Pred. No. 9.5e-60;
Matches 133; Conservative 18; Mismatches 34; Indels 11; Gaps 2;
Qy 43 BEAFQALTDPSLPSLACNVHQSVEEESKEKEGFLRTYDECVTFQPKSFRVRV 102
Db 14 EDDLDEMMDLSLPTSLFACSVHEAVFEAREQKERPEALFTYDDQVTFQPKSFRVRV 73
Qy 103 NFSHPKSAARARIELHETQFRGKPLYPFAQVOTPETDGDKLHAPPQPAKQFLISPPSS 162
Db 74 NFSKPEAAARARIELHETDFNGQKLKLYFAQ-----SYLLPPQPVKQFLISPPAS 123
Qy 163 PSVGWKPISDATPVNLNLYLAVAKLPGCEKYLHAGTSTPSVVHVCDSDMEREEDPK 222
Db 124 PPGWQKQSEDAMPVINYDLLCAVSKLPGCEKYLHAGTSTPSVVHVCESETEEBEETK 183
Qy 223 TSPKPKINOTRRPGLP 238
Db 184 -NPKQKIATRPPDP 198

RESULT 14
US-10-104-047-2892
; Sequence 2892, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2892
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2892

Query Match 50.0%; Score 648; DB 15; Length 252;
Best Local Similarity 53.4%; Pred. No. 9.2e-57;
Matches 133; Conservative 30; Mismatches 58; Indels 28; Gaps 5;
Qy 1 EFDVPRVRPRV-----LGOQASIPEDGGLFFLCCIDRDWAVTQCFAEAFQALTD 54
Db 18 EAAEAAARPGVTLRPFAPLSGAEEADGG-----DWSFIDCEME-----VLDQ 63
Qy 55 LPNSLPACNVHQSVEEESKEKEGFLRTYDECVTFQPKSFRVRINFSHPKSAAR 114
Db 64 LPSATIACHLDPRVFDGLCRAKFESLRTYDKDITFQYFKSFKRVINFSNPFSAADAR 123
Qy 115 TELHETQFRGKPLYPFAQVOTPETDGDKLHAPPQPAKQFLISPPSPSGVWKPISDAT 174
Db 124 LQLHTEFLGEMKMLYFAQTLHIGSS-----HLAPPNDKQFLISPPASPVGWKQVEDAT 179
Qy 175 PVNLNLYLAVAKLPGCEKYLHAGTSTPSVVHVCDSDMEREEDPKTS-----PKPKIN 230
Db 180 PVINYDLLVAISKLPGCEKYLHAGTSTPSVVHVCDSDQSEKEEEMERMRRPKKII 239
Qy 231 QTRRPGPLP 239
Db 240 QTRRPEYTP 248

Search completed: November 16, 2005, 16:53:29
Job time : 124.2 secs

A;Cross-references: UNIPROT:Q9P589; EMBL:AL355932; GSPDB:GN00116; NCSP:B5O22.230
A;Experimental source: BAC clone B5O22; strain OR74A
C;Genetics:
A;Gene: NCSP:B5O22.230
A;Map position: 6

Query Match 10.2%; Score 132; DB 2; Length 315;
Best Local Similarity 25.8%; Pred. No. 0.00043;
Matches 51; Conservative 26; Mismatches 91; Indels 30; Gaps 6;

QY 51 DFSDLP-----NSLFACNVHQSVPEEESKEKFEGLFRTYDECVTFQLFKSFRVR 101
DB 48 DLSNPLPSQTPPPSNLFTWNSLDVFSADNLQIRLISQTAPIFAMSPKFSFRRI 107
QY 102 INFSPKSAARIELHETQFRGKGLPLYFAQVOTPDGDKLHLAPPQAPAKQFLISPPS 161
DB 108 VTFFDEQAIAVRSVWDGEAILGERCVYFGQTPIDVSAADKHLALPDAGKLFISPPP 167
QY 162 SPVGVKWP-ISA--TPVLNYDLLYAVAKLGPGEKVELHAGTSTPSSVVHVCDSDMERE 218
DB 168 SPFHWEQRMEDAPNTMVHAEDLAELAKL-----RHHNPNNGI-----DADVK-- 211
QY 219 EDPKTSPPKPKINQTRPG 236
DB 212 --APVSPASDGGSSSRPG 227

RESULT 3
S62444
conserved hypothetical protein SPAC13G6.15c - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: hypothetical protein SPAC24B11.04c
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S62444; S62549; T37650; T38331
R;Odell, C.; Bowman, S.
submitted to the EMBL Data Library, October 1995
A;Reference number: S62430
A;Accession: S62444
A;Molecule type: DNA
A;Residues: 1-163 <ODE>
A;Cross-references: UNIPROT:Q09791; EMBL:Z54308; NID:g1008985; PIDN:CAA91108.1; PID:g100
R;Odell, C.; Churcher, C.M.
submitted to the EMBL Data Library, November 1995
A;Reference number: S62546
A;Accession: S62549
A;Molecule type: DNA
A;Residues: 1-163 <OD2>
A;Cross-references: EMBL:Z67757; NID:g1061288; PIDN:CAA91769.1; PID:g1061292
R;Odell, C.; Bowman, S.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z21734
A;Accession: T37650
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-163 <OD3>
A;Cross-references: EMBL:Z54308; PIDN:CAA91108.1; GSPDB:GN00066; SPDB:SPAC13G6.15c
A;Experimental source: strain 972h-; cosmid c13G6
R;Odell, C.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z21786
A;Accession: T38331
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-163 <OD4>
A;Cross-references: EMBL:Z67757; PIDN:CAA91769.1; GSPDB:GN00066; SPDB:SPAC24B11.04c
A;Experimental source: strain 972h-; cosmid c24B11
C;Genetics:
A;Gene: SPAC24B11.04C; SPAC13G6.15c; SPAC24B11.04c
A;Map position: 1L
C;Superfamily: fission yeast hypothetical protein SPAC13G6.15c

Query Match 7.7%; Score 99.5; DB 2; Length 163;
Best Local Similarity 33.7%; Pred. No. 0.14;

Matches 28; Conservative 13; Mismatches 29; Indels 13; Gaps 3;
QY 146 LAPPQAKQFLISPPSSVGVKPISDATP---VINYDLLYAVAKLGPGEKVELHAGTES 202
DB 85 LQVPKEFNWLISSPPSPVGVMEPIVESPNSQLAHDIQLKLDLGNALLNDHSAG--- 141
QY 203 TPSVVHVCDSDMEREDPKTSP 225
DB 142 -PQIVI-----SEHNNTKETSP 157

RESULT 4
A72203
cellobiose-phosphorylase - Thermotoga maritima (strain MSBB)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: A72203
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke;
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: A72203
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-813 <ARN>
A;Cross-references: UNIPROT:Q9X2G3; GB:AE001822; GB:AE000512; NID:g4982429; PIDN:AAD3691
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1848

Query Match 7.2%; Score 93.5; DB 2; Length 813;
Best Local Similarity 22.2%; Pred. No. 3.7;
Matches 58; Conservative 40; Mismatches 112; Indels 51; Gaps 12;

QY 2 FVDPVRPRVRLGQOASIPED--GGLFPLCCIDRD--WAVT-----QCTAEEAFQALT 50
DB 47 YKDARLR-RITFRYNNVPTDAGGRFYFIREENGDFWFTPTWMPVRKOLSPFEARHGLGYT 105
QY 51 DFSDLPNSL-----FACNVHQSVPEEESKEKFEGLFRTYDECVTFQL--FKSF 97
DB 106 KITGERNGLRATITFYVPRHPTGEVHYLVLENKAEKPKIKLFSFIEFCLNWDMDTNF 165
QY 98 RRVRFNSHPKSAARIELHETQFRGKGLPLYFAQVQTP-----ETDGDK-LHLAPPQPA 152
DB 166 QR--NYSTGEVEIEGSIYHKTEYRRNRHYAFVSVNQPIDGPTDRESFGLYSGFEA 222
QY 153 KQFLI--SPSPSPVGVKPISDATPVLNYDLLYAVAKLGPGEKVELHAGTSTPSSVVHV 210
DB 223 PQAVVEGKPRNSVAGWAPIASH-----YLEIELAPSEKKEL-----IFILGYV 266
QY 211 CDSDMEREEDPKTSPKPKINQ 231
DB 267 ENPBEKWEKPGVINKKRAKE 287

RESULT 5
T32952
hypothetical protein C15B6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
R;Rohlfing, T.; Biewald, T.
submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid C15E6.
A;Reference number: Z21253
A;Accession: T32952
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-428 <ROH>
A;Cross-references: EMBL:AF045636; PIDN:AAC02559.1; GSPDB:GN00022; CBSP:C15B6.1
A;Experimental source: strain Bristol N2; clone C15B6

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C/Accession: C96534
C/R/Oeologts, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurose, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.I.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: AB6141; MUID:21016719; PMID:11130712

A/Accession: C96534

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-671 <STO>

A/Cross-references: UNIPROT:Q9FXA2; GB:AE005173; NID:g10120431; PIDN:AAG13056.1; GSPDB:I:
C/Genetics:

A/Gene: F14J22.3

A/Map position: 1

C/Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

Query Match 7.0%; Score 91; DB 2; Length 671;
Best Local Similarity 21.3%; Pred.No. 4.8;
Matches 51; Conservative 38; Mismatches 100; Indels 50; Gaps 12;

Qy 32 DRDWAQTQC-----FAEERAFQALTFPSDLTP--NSLFACNVHVSVPFEESKSKFEG 80
Db 291 DKSNFWGKAQKKSERETELKQKEQSLSKEADKSQSNLYVKVLDES-VTDDKLREHF-A 348
Qy 81 LFRTYDECVTTLFKSRRVR---INFSGPKSAARIELHETFRKKL---PLYPAVQV 135
Db 349 PFGTITTSCKVMRDPGVSRSGVFASFTEPEATRA-----ITEMNGKMIVTKPLYYALAQ 403
Qy 136 TPPTDGDGLHL-----APPQAKQFLISPPSSPVCWK-----PISDATPVLN 179
Db 404 RKEDRKARLAQAQSQMRPNMPPAVCFRMQMTYPCGGPHMQQLFYCGGPPAMTPQFGY 463
Qy 180 DLLAYAVAKLGPKBYELHAGTESTPSVVHVCDSDMERBEDPKTSPKPKNOTRRPGLP 238
Db 464 Q-----QLLVPG----MRPGSGPMFPFMFMQGGQQGQQGQQGQQGQP--GGRRRALP 511

```

N;Alternate names: ksr connector enhancer protein
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13160
R;Therrien, M.; Wong, A.M.; Rubin, G.M.
Cell 95, 343-353, 1998
A;Title: CNK, a RAF-binding multidomain protein required for RAS signaling.
A;Reference number: Z17616; MUID:99029842; PMID:9814705
A;Accession: T13160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1557 <THE>
A;Cross-references: UNIPROT:O96652; EMBL:AF100152; NID:g3930778; PID:g3930779; PIDN:AAC
C;Genetics:
A;Cross-references: FlyBase:FBgn0021818
C;Function:
A;Description: regulates RAF function and/or targets RAF to a specific subcellular comp

Query Match 7.0%; Score 90.5; DB 2; Length 1557;
Best Local Similarity 24.2%; Pred. No. 15;
Matches 47; Conservative 22; Mismatches 76; Indels 49; Gaps 8;

Qy 46 FQALTFPSDLPLNSLPACNVHQSVFEE-----SKEKEGLRTVD 86
Db 511 FDAKEDYV-MKNKPKFICNVNTILETFEPIPFADGDEDALETLRNCKTENABELLEAN 569

```


Db 313 -----GQWKYNAIGTSSTPT-----STVTPTPTPTPTPTPTVTAATPTPTP 357

RESULT 14

T42761

Basoon protein - rat

N:Alternate names: brain-specific synapse-associated protein

C:Species: Rattus norvegicus (Norway rat)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T42761

R:Dieck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex J. Cell Biol. 142, 499-509, 1998

A:Title: Basoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localize

A:Reference number: Z22249; MUID:98345363; PMID:9679147

A:Accession: T42761

A:Status: preliminary;

A:Molecule type: mRNA

A:Residues: 1-3938 <DIE>

A:Cross-references: UNIPROT:O88778; EMBL:Y16563; MID:g3413503; PIDN:CAA76287.1; PID:g34

A:Experimental source: strain Sprague Dawley; brain

C:Function:

A:Description: may be involved in cytomatrix organization at the site of neurotransmitt

A:Note: Component of the presynaptic cytoskeleton

C:Keywords: coiled coil; zinc finger

Query Match 6.7%; Score 86.5; DB 2; Length 3938;

Best Local Similarity 30.4%; Pred. No. 1.1e+02;

Matches 34; Conservative 15; Mismatches 40; Indels 23; Gaps 7;

QY 132 AQQTPTDGDGLHLAPPQAKOFLISPPSSPSGVGKPISDATPVNLNLYAVAKLGP 191

DB 1441 ASREKPLUSGGDG-EVGPPQPSRGYSYFTGSP-----PLSPSTP--SESPTFSKLGP 1492

QY 192 ERYELHAGTES-TFSVVVHVHCDSDMEREDPKTSPKPKINQ-----TRRPGLP 238

DB 1493 ATAESTTQTSPLTFS-----SDIPRSVG---TPSPMVAQGQTTPHRPSTP 1534

RESULT 15

A88852

protein unc-22 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: A88852

R:anonymous, The C. elegans Sequencing Consortium.

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_e

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an

A:Accession: A88852

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-6831 <STO>

A:Cross-references: UNIPROT:Q23550; GB:chr_IV; PIDN:CAA98081.1; PID:g33881830; GSPDB:GNO

C:Genetics:

A:Gene: unc-22

A:Map position: 4

C:Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homology;

Query Match 6.7%; Score 86.5; DB 2; Length 6831;

Best Local Similarity 20.3%; Pred. No. 2.2e+02;

Matches 65; Conservative 28; Mismatches 102; Indels 125; Gaps 13;

QY 35 WAYTQFAEEAFOALTFDSDLPNLSF-----ACNVHQSVEEESKEKF---- 78

DB 3856 WTVGDSGAALAPPELLVDAKSSTTSIFPSAKRADSGNYKLVKVKELGDEAIFEVIVQDR 3915

QY 79 -----EGLFR-----TYDECVTFFQLFKSRVRINFSHPKSAARAIHELHQTFRGKK----- 126

DB 3916 PSAEPGLEVSVDYTKDSCV-----LNWPKPDGGGAEISNYVVEKRDTKNTW 3963

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QY      127 LPL-----YFAQVQTPETDG--DKLHLAPPQPAKQFLISP--PSSP 163
Db      3964 VPSAFVTGTSITVPKLTGHEYEFVRVMAENTFGRSDSLNTDPEVLAKDPFGTGGKGRP 4023
QY      164 -----SYGWKPISD--ATPVLNYDL----- 181
Db      4024 EIVDTDNHDIDIKNDPPRDNGGSPVDHYDIERKDAKTGEWIKVNTSPVQGTAFSDTRVQK 4083
QY      182 -----LYAVAKLGFGEKYLHAGTESTPSVVHVHVCSDMEREE-----DP----- 221
Db      4084 GHTYEYRVVAVNKAQGPQPSDSSAAATAKPMHEAPKFOLDLDGKEFRVKAGEPLVITIPF 4143
QY      222 KTSXPKINQTRRPGLPPEG 241
Db      4144 TASPOPDISWTKEGKPLAG 4163
```

Search completed: November 16, 2005, 17:13:07
Job time : 15.85 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:32:05 ; Search time 60.5 Seconds
(without alignments)
2048.317 Million cell updates/sec

Title: US-09-575-580B-5
Perfect score: 1296
Sequence: 1 BFVDRVRPRVRLGQASIP.....TSPKPKINQTRRPLPPFGH 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1186	91.5	243	2 Q8VIP4	Q8vip4 mus musculus
2	1176	90.7	243	2 Q8CH26	Q8ch26 rattus norv
3	1116	86.1	243	2 Q8N116	Q8n116 homo sapien
4	882	68.1	197	1 CC2P_MOUSE	Q9jhg2 mus musculus
5	876	67.6	197	2 Q8CH27	Q8ch27 rattus norv
6	868	67.0	192	2 Q8VIP5	Q8vip5 mus musculus
7	861	66.4	225	2 Q86YJ0	Q86y10 homo sapien
8	848	65.4	197	1 CC2P_HUMAN	Q14206 homo sapien
9	725	55.9	195	2 Q6NSN4	Q6nsn4 brachydanio
10	720.5	55.6	239	1 CC3P_MOUSE	Q9jkk0 mus musculus
11	708.5	54.7	241	1 CC3P_HUMAN	Q9uka8 homo sapien
12	702	54.2	230	2 Q6DG39	Q6dg39 brachydanio
13	648	50.0	252	2 Q72555	Q72555 homo sapien
14	632	48.8	251	2 Q7TNY3	Q7tny3 mus musculus
15	617	47.6	197	1 CC1P_CRIGR	Q35847 cricetus
16	616	47.5	197	1 CC1P_HUMAN	P53805 homo sapien
17	616	47.5	199	2 Q6IN33	Q6in33 rattus norv
18	615	47.5	197	2 Q6XXM7	Q6xxm7 ovis aries
19	614	47.4	199	2 Q8K4S2	Q8k4s2 rattus norv
20	608.5	47.0	198	1 CC1P_MOUSE	Q9jhg6 mus musculus
21	589	45.4	199	2 Q7T0U1	Q7t0u1 xenopus lae
22	588	45.4	199	2 Q6DK90	Q6dk90 xenopus tro
23	582	44.9	242	2 Q6ZMM3	Q6zmm3 homo sapien
24	579	44.7	231	2 Q7ZXP4	Q7zxp4 xenopus lae
25	540	41.7	196	2 Q6DGB1	Q6dgb1 brachydanio
26	522.5	40.3	210	2 Q6DC33	Q6dc33 brachydanio
27	418.5	32.3	292	1 SRA_DROME	Q9xz18 drosophila
28	330.5	25.5	207	1 CCPL_CABEL	P53806 caenorhabdi
29	132	10.2	315	2 Q9P5S9	Q9p5s9 neurospora
30	121.5	9.4	249	2 Q66PG0	Q66pg0 cryptococcu
31	116.5	9.0	249	2 Q9P4A1	Q9p4a1 cryptococcu

ALIGNMENTS

RESULT 1

ID	Q8VIP4	PRELIMINARY;	PRT;	243 AA.
AC	Q8VIP4;			
DT	01-MAR-2002 (Tremblrel. 20, Created)			
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)			
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE	Calcineurin inhibitory protein ZAKI-4 beta.			
GN	Name=Descr11; Synonyms=ZAKI-4 beta;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kanou Y., Miyazaki T., Seo H., Murata Y.;			
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB061525; BAB71956.1; -			
DR	MGD; MGI:1858219; Descr11.			
DR	GO; GO:0019722; P:calcium-mediated signaling; IEA.			
DR	Fiam; PF04847; Calcipressin; 1.			
SQ	SEQUENCE 243 AA; 27332 MW; 2CD8CIA810291851 CRC64;			

Query Match	91.5%;	Score 1186;	DB 2;	Length 243;
Best Local Similarity	98.2%;	Pred. No. 8.8e-93;		
Matches	223;	Conservative	0;	Mismatches 4;
Indels	0;	Gaps	0;	
Qy	13	LQQQASIPEDGGLFLCCIDRDWAVTQCFABEAFQALTDPSDLNLSLFCACNVHQSVFEE	72	
Db	13	LQQQASIPEDGGLFLCCIDRDWAVTQCFABEAFQALTDPSDLNLSLFCACNVHQSVFEE	72	
Qy	73	ESKEKEGLFRFYDSCVTFQLEKSFRRVRINFSHPKSAARARIELHETQFRGKKLPLYFA	132	
Db	73	ESKEKEGLFRFYDSCVTFQLEKSFRRVRINFSHPKSAARARIELHETQFRGKKLPLYFA	132	
Qy	133	QVQTETDGDGLHAPPQAPAKFLISPPSSPVGVKPKISDAPVNLNLLYAVAKLPGGE	192	
Db	133	QVQTETDGDGLHAPPQAPAKFLISPPSSPVGVKPKISDAPVNLNLLYAVAKLPGGE	192	
Qy	193	KYELHAGTESTPSVVHVHVCDSMEEREEDPKTSPKPKINQTRRPLPP	239	
Db	193	KYELHAGTESTPSVVHVHVCDSMEEREEDPKTSPKPKIITRRPGLPP	239	

RESULT 2

ID	Q8CH26	PRELIMINARY;	PRT;	243 AA.
AC	Q8CH26;			
DT	01-MAR-2003 (Tremblrel. 23, Created)			
DT	01-MAR-2003 (Tremblrel. 23, Last sequence update)			
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE	ZAKI-4 beta.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RA Miyazaki T., Cao X., Kambe F., Ohmori S., Seo H.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF459023; AAO1554.1; -.
DR GO; GO:0019722; P:calcium-mediated signaling; IEA.
DR InterPro; IPR006931; Calcipressin.
DR Pfam; PF04847; Calcipressin; 1.
SQ SEQUENCE 243 AA; 27311 MW; 00E05BD1DCD0492D CRC64;

Query Match 90.7%; Score 1176; DB 2; Length 243;
Best Local Similarity 96.5%; Pred. No. 6.2e-92;
Matches 219; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 13 LQQASIPEDGGLFLCCIDRDWAVTQCFAEAFQALTFDPSLPSLFCACNVHQSVFEE 72
Db 13 LQQASVPEDGGLFLCCIDRDWAVTQCFAEAFQALTFDPSLPSLFCACNVHQSVFEE 72

QY 73 ESKEFEGFLRTYDECVTFLQFKSFRVRINFSHPKSAARARIELHETQFRGKKLPLFYA 132
Db 73 ESKEFEGFLRTYDECVTFLQFKSFRVRINFSHPKSAARARIELHETQFRGKKLPLFYA 132

QY 133 QVQTPETDGDKLHLAPPQPAKQFLISPPSSVGVWPKIPSDATPVLNLDLYAVAKLGPGE 192
Db 133 QVQTPETDGDKLHLAPPQPAKQFLISPPSSVGVWPKIPSDATPVLNLDLYAVAKLGPGE 192

QY 193 KYELHAGTESPVSVVHVCDSDMEREDPKTSPKPKINQTRRPLPP 239
Db 193 KYELHAGTESPVSVVHVCDSDLEBEDPKTSPKPKIIQTRRPLPP 239

RESULT 3
Q8N116 PRELIMINARY; PRT; 243 AA.
AC Q8N116;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Calcineurin inhibitor ZAKI-4 beta splice variant 1 (Calcineurin
DE inhibitor ZAKI-4 beta splice variant 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22250686; PubMed=12102656; DOI=10.1042/BJ20011797;
RA Cao X., Kambe F., Miyazaki T., Sarkar D., Ohmori S., Seo H.;
RT "Novel human ZAKI-4 isoforms: hormonal and tissue-specific regulation
RT and function as calcineurin inhibitors."
RL Biochem. J. 367:459-466(2002).
DR EMBL; AY034085; AAK59805.1; -.
DR EMBL; AY034086; AAK59806.1; -.
DR GO; GO:0019722; P:calcium-mediated signaling; IEA.
DR InterPro; IPR006931; Calcipressin.
DR Pfam; PF04847; Calcipressin; 1.
SQ SEQUENCE 243 AA; 27247 MW; 780073AE29A973E4 CRC64;

Query Match 86.1%; Score 1116; DB 2; Length 243;
Best Local Similarity 91.6%; Pred. No. 7.9e-87;
Matches 207; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 14 GQASIPEDGGLFLCCIDRDWAVTQCFAEAFQALTFDPSLPSLFCACNVHQSVFEE 73
Db 14 GQASVPEDGGLFLCCIDRDWAVTQCFAEAFQALTFDPSLPSLFCACNVHQSVFEE 73

QY 74 SKEFEGFLRTYDECVTFLQFKSFRVRINFSHPKSAARARIELHETQFRGKKLPLFYA 133
Db 74 SKEFEGFLRTYDVCVTFLQFKSFRVRINFSHPKSAARARIELHETQFRGKKLPLFYA 133
```

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QY 134 VQTPETDGDKLHLAPPQPAKQFLISPPSSVGVWPKIPSDATPVLNLDLYAVAKLGPGEK 193
Db 134 VQTPETDGDKLHLAPPQPAKQFLISPPSSVGVWPKIPSDATPVLNLDLYAVAKLGPGEK 193

QY 194 YELHAGTESPVSVVHVCDSDMEREDPKTSPKPKINQTRRPLPP 239
Db 194 YELHAGTESPVSVVHVCDSDIEBEDPKTSPKPKIIQTRRPLPP 239

RESULT 4
CCP2_MOUSE STANDARD; PRT; 197 AA.
ID CCP2_MOUSE
AC Q9JHG2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcipressin 2 (Down syndrome candidate region 1-like protein 1)
DE (Myocyte-enriched calcineurin interacting protein 2) (MCIP2).
GN Name=DSCR11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20187590; PubMed=10722714; DOI=10.1074/jbc.275.12.8719;
RA Rothermel B., Vega R.B., Yang J., Wu H., Bassel-Duby R.,
RA Williams R.S.;
RT "A protein encoded within the Down syndrome critical region is
RT enriched in striated muscles and inhibits calcineurin signaling."
RL J. Biol. Chem. 275:8719-8725(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=20534792; PubMed=11080588; DOI=10.1016/S0378-1119(00)00407-8;
RA Strippoli P., Petrini M., Lenzi L., Carinci P., Zannotti M.;
RT "The murine DSCR1-like (Down syndrome candidate region 1) gene family:
RT conserved synteny with the human orthologous genes."
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner S.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Inhibits calcineurin-dependent transcriptional responses
CC by binding to the catalytic domain of calcineurin A. Could play a
CC role during central nervous system development.
CC -!- TISSUE SPECIFICITY: Highest expression in heart, skeletal muscle
CC and brain. Lower expression in all other tissues.
CC -!- SIMILARITY: Belongs to the DSCR1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration -
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC -----
```



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QY 28 LCICDRDQWAVTQCPA--EEAFQALTFDPSLPSLFAACNVHQSVFBEESKEKFEGLFRTY 85
Db 16 LCSSDQEEBEEVMFGENEDGLEMDLSLPTSLFACSVHEAVFEVQEKERFEALFTLY 75

QY 86 DCVTFQLFKSPRRVRINFSHPKSAARARIELHETQFGKPLPLFAQVOTPETDGDKLH 145
Db 76 DDQVTFQLFKSPRRVRINFSHPKSAARARIELHSEFGRKLLPLFAQVQVSGEARDKSY 135

QY 146 LAPPQPAKQFLISPPSSPVGKPISDATPVLYNDLLYAVAKLPGGKGYELHAGTESPTS 205
Db 136 LLPQVQKQFLISPPASPPVGMKQSEDAMPVINYDLLCAVSKLPGGKGYELHAGTESPTS 195

QY 206 VVVHVCSDMEREDPKTSPPKINQTRRPGLP 238
Db 196 VVVHVCSETEBEEETK-NPKQKITQTRRPEAP 227

RESULT 11
CCP3 HUMAN
ID CCP3 HUMAN STANDARD; PRT; 241 AA.
AC Q9UKA8; Q9NUC8; Q9UKA7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcipressin.3 (Down syndrome candidate region 1-like protein 2)
DE (Myocyte-enriched calcineurin interacting protein 3) (MCIP3).
GN Name=DSCRIL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX TISSUE=Peripheral blood, and Placenta;
RX MEDLINE=2021370; PubMed=10756093; DOI=10.1006/geno.2000.6127;
RA Strippoli P., Lenzi L., Petriani M., Carinci P., Zannotti M.;
RT "A new gene family including DSCR1 (Down syndrome candidate region 1)
RT and ZAK1-4: characterization from yeast to human and identification of
RT DSCR1-like 2, a novel human member (DSCRIL2).";
RL Genomics 64:252-263(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE=Brain;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.N., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blacklesley R.W., Touchwood J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 66-241 FROM N.A.
RA Bagguley C.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Inhibits calcineurin-dependent transcriptional responses
CC by binding to the catalytic domain of calcineurin A. Could play a
CC role during central nervous system development (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;

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CC CC Name=1;
CC CC IsoId=Q9UKA8-1; Sequence=Displayed;
CC CC Name=2;
CC CC IsoId=Q9UKA8-2; Sequence=VSP 001319;
CC CC -!- TISSUE SPECIFICITY: Highest expression in heart, skeletal muscle
CC CC kidney, liver and peripheral blood leukocytes. Lower expression in
CC CC all other tissues.
CC CC -!- SIMILARITY: Belongs to the DSCR1 family.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; AF176116; AAF01684.1; -
CC CC EMBL; AF176117; AAF01685.1; -
CC CC EMBL; BC035854; AAH35854.1; -
CC CC EMBL; AL034582; CAB72298.1; -
CC CC MIM; 605860; -
CC CC GO; GO:0003723; F:RNA binding; TAS.
CC CC GO; GO:0009653; P:morphogenesis; TAS.
CC CC InterPro; IPR006931; Calcipressin.
CC CC InterPro; IPR009078; Ferritin/RR_like.
CC CC Pfam; PF04847; Calcipressin; 1.
CC CC KW Alternative splicing.
CC CC FT VARSPLOC 124 133 Missing (in isoform 2).
CC CC FT FTID=VSP_001319.
CC CC SQ SEQUENCE 241 AA; 27492 MW; 91AB619F5E443FBD CRC64;

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Matches 141; Conservative 20; Mismatches 49; Indels 3; Gaps 2;

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Db 16 LCSSDQEEBEEVMFGENEDGLEMDLSLPTSLFACSVHEAVFEVQEKERFEALFTLY 75

QY 86 DCVTFQLFKSPRRVRINFSHPKSAARARIELHETQFGKPLPLFAQVOTPETDGDKLH 145
Db 76 DDQVTFQLFKSPRRVRINFSHPKSAARARIELHSEFGRKLLPLFAQVQVSGEARDKSY 135

QY 146 LAPPQPAKQFLISPPSSPVGKPISDATPVLYNDLLYAVAKLPGGKGYELHAGTESPTS 205
Db 136 LLPQVQKQFLISPPASPPVGMKQSEDAMPVINYDLLCAVSKLPGGKGYELHAGTESPTS 195

QY 206 VVVHVCSDMEREDPKTSPPKINQTRRPGLP 238
Db 196 VVVHVCSETEBEEETK-NPKQKITQTRRPPDP 227

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AC Q6DG39;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
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RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heideh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grichwood J., Schmutz J., Myers J.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [12]
RC TISSUE=Whole;
RC Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076514; AAH76514.1; -;
DR GO; GO:0019722; P:calcium-mediated signaling; IEA.
DR InterPro; IPR006931; Calciopressin.
DR Pfam; PF04847; Calciopressin; 1.
KW Hypothetical protein.
SQ SEQUENCE 230 AA; 26123 MW; B1D19EB6D3A3460B CRC64;

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Best Local Similarity 67.5%; Pred. No. 1.2e-51;
Matches 133; Conservative 26; Mismatches 36; Indels 2; Gaps 1;
ID Q72555 PRELIMINARY; PRT; 252 AA.
AC Q72555;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calciopressin 1 large isoform.
GN Name=DSCL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=22806131; PubMed=12809556; DOI=10.1042/BJ20030267;
RA Genesca L., Aubareda A., Fuentes J.J., Estivill X., de la Luna S.,
RA Perez-Riba M.;
RT "Phosphorylation of calcipressin 1 increases its ability to inhibit
RT calcineurin and decreases calcipressin half-life.";
RL Biochem. J. 374:567-575 (2003).
DR EMBL; AY325904; AAP96744.1; -;
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR006931; Calciopressin.
DR Pfam; PF04847; Calciopressin; 1.
SQ SEQUENCE 251 AA; 28137 MW; 09F47C73D847FB2B CRC64;

Query Match 48.8%; Score 632; DB 2; Length 251;
Best Local Similarity 53.6%; Pred. No. 1.2e-45;
Matches 133; Conservative 28; Mismatches 63; Indels 24; Gaps 5;
ID Q72555 PRELIMINARY; PRT; 251 AA.
AC Q72555;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calciopressin 1 large isoform.
GN Name=DSCL1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RP SEQUENCE FROM N.A.
RC STRAIN=NIH/Swiss;
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RA Genesca L., Aubareda A., Fuentes J.J., Estivill X., de la Luna S.,
RA Perez-Riba M.;
RT "Phosphorylation of calcipressin 1 increases its ability to inhibit
RT calcineurin and decreases calcipressin half-life.";
RL Biochem. J. 374:567-575 (2003).
DR EMBL; AY325904; AAP96744.1; -;
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR006931; Calciopressin.
DR Pfam; PF04847; Calciopressin; 1.
SQ SEQUENCE 251 AA; 28137 MW; 09F47C73D847FB2B CRC64;

Query Match 54.2%; Score 702; DB 2; Length 230;
Best Local Similarity 67.5%; Pred. No. 1.2e-51;
Matches 133; Conservative 26; Mismatches 36; Indels 2; Gaps 1;
ID Q72555 PRELIMINARY; PRT; 252 AA.
AC Q72555;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calciopressin 1 large isoform.
GN Name=DSCL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RC TISSUE=Heart;
RX MEDLINE=22806131; PubMed=12809556; DOI=10.1042/BJ20030267;
RA Genesca L., Aubareda A., Fuentes J.J., Estivill X., de la Luna S.,
RA Perez-Riba M.;
RT "Phosphorylation of calcipressin 1 increases its ability to inhibit
RT calcineurin and decreases calcipressin half-life.";
RL Biochem. J. 374:567-575 (2003).
RN [12]
RC TISSUE=Whole;
RC Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076514; AAH76514.1; -;
DR GO; GO:0019722; P:calcium-mediated signaling; IEA.
DR InterPro; IPR006931; Calciopressin.
DR Pfam; PF04847; Calciopressin; 1.
KW Hypothetical protein.
SQ SEQUENCE 230 AA; 26123 MW; B1D19EB6D3A3460B CRC64;

DR EMBL; AY325903; AAP96743.1; -;
DR GO; GO:0019722; P:calcium-mediated signaling; IEA.
DR InterPro; IPR006931; Calciopressin.
DR Pfam; PF04847; Calciopressin; 1.
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AC Q72555;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calciopressin 1 large isoform.
GN Name=DSCL1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RC STRAIN=NIH/Swiss;
RX MEDLINE=22806131; PubMed=12809556; DOI=10.1042/BJ20030267;
RA Genesca L., Aubareda A., Fuentes J.J., Estivill X., de la Luna S.,
RA Perez-Riba M.;
RT "Phosphorylation of calcipressin 1 increases its ability to inhibit
RT calcineurin and decreases calcipressin half-life.";
RL Biochem. J. 374:567-575 (2003).
DR EMBL; AY325904; AAP96744.1; -;
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR006931; Calciopressin.
DR Pfam; PF04847; Calciopressin; 1.
SQ SEQUENCE 251 AA; 28137 MW; 09F47C73D847FB2B CRC64;

Query Match 48.8%; Score 632; DB 2; Length 251;
Best Local Similarity 53.6%; Pred. No. 1.2e-45;
Matches 133; Conservative 28; Mismatches 63; Indels 24; Gaps 5;
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AC Q72555;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calciopressin 1 large isoform.
GN Name=DSCL1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RC STRAIN=NIH/Swiss;
RX MEDLINE=22806131; PubMed=12809556; DOI=10.1042/BJ20030267;
RA Genesca L., Aubareda A., Fuentes J.J., Estivill X., de la Luna S.,
RA Perez-Riba M.;
RT "Phosphorylation of calcipressin 1 increases its ability to inhibit
RT calcineurin and decreases calcipressin half-life.";
RL Biochem. J. 374:567-575 (2003).
DR EMBL; AY325904; AAP96744.1; -;
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR006931; Calciopressin.
DR Pfam; PF04847; Calciopressin; 1.
SQ SEQUENCE 251 AA; 28137 MW; 09F47C73D847FB2B CRC64;

Query Match 54.2%; Score 702; DB 2; Length 230;
Best Local Similarity 67.5%; Pred. No. 1.2e-51;
Matches 133; Conservative 26; Mismatches 36; Indels 2; Gaps 1;
ID Q72555 PRELIMINARY; PRT; 252 AA.
AC Q72555;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calciopressin 1 large isoform.
GN Name=DSCL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=22806131; PubMed=12809556; DOI=10.1042/BJ20030267;
RA Genesca L., Aubareda A., Fuentes J.J., Estivill X., de la Luna S.,
RA Perez-Riba M.;
RT "Phosphorylation of calcipressin 1 increases its ability to inhibit
RT calcineurin and decreases calcipressin half-life.";
RL Biochem. J. 374:567-575 (2003).
RN [12]
RC TISSUE=Whole;
RC Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076514; AAH76514.1; -;
DR GO; GO:0019722; P:calcium-mediated signaling; IEA.
DR InterPro; IPR006931; Calciopressin.
DR Pfam; PF04847; Calciopressin; 1.
KW Hypothetical protein.
SQ SEQUENCE 230 AA; 26123 MW; B1D19EB6D3A3460B CRC64;

Db 124 LHKTEFLGKEMKLYFAQTUHGSS : ||||| | ||||| : ||||| : ||||| 179
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Db 180 INYDLLYALSKLPGKEKYLHAAATDTPSVVVHVHVCDSQENEEEBEEMERMKRPKPKLIQ 239
QY 232 TRRPGGLPP 239
Db 240 TRPEYTP 247

Search completed: November 16, 2005, 17:12:35
Job time : 61.5 secs

RESULT 15
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AC O35847;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcipressin 1 (Down syndrome critical region protein 1 homolog)
DE (Oxidative-induced protein Adapt78).
GN Name=DSCR1; Synonyms=ADAPT78;
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97329095; PubMed=9185608; DOI=10.1006/abbi.1997.0109;
RA Crawford D.R., Leahy K.P., Abramova N., Lan L., Wang Y., Davies K.J.;
RT "Hamster adapt78 mRNA is a Down syndrome critical region homologue
that is inducible by oxidative stress.";
RL Arch. Biochem. Biophys. 342:6-12(1997).
CC -!- FUNCTION: Inhibits calcineurin-dependent transcriptional responses
by binding to the catalytic domain of calcineurin A. Could play a
role during central nervous system development (By similarity).
CC -!- INDUCTION: By oxidative stress.
CC -!- SIMILARITY: Belongs to the DSCR1 family.

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or send an email to license@isb-sib.ch).

DR EMBL; U60263; AB368517.1; -
DR InterPro; IPR006931; Calcipressin.
DR Pfam; PF04847; Calcipressin; 1.
SQ SEQUENCE 197 AA; 22674 MW; 0EFC68FPA55826439 CRC64;

Query Match 47.6%; Score 617; DB 1; Length 197;
Best Local Similarity 62.2%; Pred. No. 1.7e-44;
Matches 120; Conservative 26; Mismatches 39; Indels 8; Gaps 2;

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Db 5 DFNYNFSSLIACVANGDVFESESETRAKFESLRTYDITQYFKSKRVRFNSPLSA 64

QY 111 ABARIELHETQPRGKLPYFAQVOTPETDGDKLHAPPQAKQFLISPPSPSVGWKPI 170
Db 65 ADARLQLHKTEFLGKEMKLYFAQTUHGSS ----HLAPPNPKQFLISPPASPPVGVKQV 120

QY 171 SDATPVLNVDLLYAVAKLPGKEKYLHAGTSTPSVVHVHVCDSMDEREEDPKTS----PK 226
Db 121 EDATPVINYDLLYALSKLPGKEKYLHAAATDTPSVVVHVHVCDSQENEEEBEEMERMKRPK 180

QY 227 PKINQTRRPGGLPP 239
Db 181 PKIIQTRRPEYTP 193